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54 **Immobilized protein G variants and the use thereof.**

57 Protein G variants and processes for their preparation by recombinant techniques are disclosed, as well as use of the same technology to make known Protein G. Such variants are useful for separating IgG and fragments thereof.

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IMMOBILIZED PROTEIN G VARIANTS AND THE USE THEREOF

This present invention relates to immobilized Protein G variants and the use thereof.

There has been growing interest in recent years in bacterial Ig (immunoglobulin) receptors, molecules that bind to antibodies through a nonimmune mechanism. This binding is not to the antigen recognition site, which is located in the variable portion of the antibody molecule, but to the constant portion of the antibody. The constant region is common to many types of antibodies, thus bacterial Ig receptors can bind to many types of antibodies. This property makes bacterial Ig receptors useful in a number of immunochemical applications.

Bacterial Ig receptors have a number of useful or potentially useful applications, primarily in the detection of antibodies, the purification of antibodies and the treatment of diseases. The detection of antibodies is required in several phases of laboratory research in immunology, including the screening of hybridoma clones for the secretion of specific monoclonal antibodies, the measurement of the immune response of an immunized animal, and the quantitation of antigens by competitive binding assays. Methods for detecting antibodies using bacterial Ig receptors have been found to be more sensitive and less prone to interference and high background signals than other detection methods [Boyle, M.D.P., *Biotechniques* 2:334-340 (1984)].

Ig receptors also are useful in purifying antibodies to be used in the purification of protein drugs and as therapeutics. Although a number of methods are known, a popular method involves the use of affinity chromatography on columns of immobilized bacterial Ig receptors. This method is preferred because the columns can be reused many times, thus lowering the expense of purification.

A number of potential clinical uses of bacterial Ig receptors are currently under investigation. They include passing plasma over extracorporeal columns of immobilized Ig receptors, then reinfusing the treated plasma. See, for example, Tenan, D.S., et al., *N. Eng. J. Med.* 305 :1195-1200 (1981).

The best known bacterial Ig receptor is Protein A of *Staphylococcus aureus*, which binds to the constant F_c domain of immunoglobulin IgG. Other bacterial Ig receptors also have been identified. One of these is known as Protein G of Group G streptococci. Although Protein G is analogous to Protein A, Protein G has several important advantages. For example, Protein G binds to all subclasses of human IgG, whereas Protein A does not bind to the IgG3 subclass [Reis, K. J. et al. *J. Immunol.* 132 :3098-3102 (1984)]. Protein G also is specific for IgG and does not cross-react with human antibodies of type IgA and IgM as Protein A does. [Myhre, E.B. and Kronvall, G. "Immunoglobulin Specificities of Defined Types of Streptococcal Ig Receptors" In : *Basic Concepts of Streptococci and Streptococcal Diseases* ; J.E. Holm and P. Christensen, eds.; Redbook, Ltd., Chertsey, Surrey; pp. 209-210 (1983)]. In addition, Protein G binds to certain animal IgGs to which Protein A binds weakly or not at all. These include bovine, ovine, and caprine IgG and several subclasses of equine IgG (Reis, K. J. et al., *supra*). Protein G also has been found superior to Protein A in binding to several subclasses of murine monoclonal antibodies [Bjorck, L. and Kronvall, G. *J. Immunol.* 133 :969-974 (1984)]. For these reasons, Protein G is likely to become the bacterial Ig receptor of choice in a variety of applications.

Protein G may be obtained for study by purification from Streptococcal strains which naturally produce it. For example, Streptococcal cells have been treated with proteolytic enzymes (e.g., papain or trypsin) to solubilize the Protein G (which is a cell wall protein), followed by known protein purification procedures (e.g., ion exchange chromatography, gel filtration, and affinity chromatography) to further purify the Protein G (European Patent Application, Publication Number 0 131 142).

Thus the present invention in its broadest terms addresses the advantages, uses and potential uses of Protein G and variants thereof. It is appreciated that it would be desirable to be able to produce such variants using recombinant DNA methodology and to immobilize the variants for use in chromatography. Accordingly, it is an object of the present invention to construct and clone genes encoding Protein G and variants thereof and to produce Protein G and variants thereof by transforming a microbial host with the cloned gene and cultivating the host under Protein G-producing conditions. It is also an object of the present invention to immobilize Protein G and variants thereof on solid supports and to use the immobilized variants in chromatographic separation processes.

Thus a first of the present invention relates to a nucleic acid sequence encoding for Protein G or a Protein G variant.

A second aspect of the present invention relates to a nucleic acid sequence encoding for an active binding site or a portion thereof of Protein G or a Protein G variant.

Thus in its broadest terms, the invention in a third encompasses recombinant Protein G or a variant thereof.

To these ends, the invention in a fourth aspect covers a vector comprising a nucleic acid sequence encoding for Protein G or a variant of Protein G, or an active binding site thereof. The vector is preferably lambda gt11, m13mp9, pBR322 or pGx1066.

A fifth aspect of the invention relates to a host transfected with the vector of the fourth aspect. The host is preferably *E. coli* or *Bacillus subtilis*.

A sixth aspect of the present invention relates to a Protein G variant.

It will be appreciated that preferred features and characteristics of one aspect of the present invention are as for another aspect *mutatis mutandis*.

The invention is directed to immobilized Protein G variants on a solid phase support and the use thereof. In particular, the invention also is directed to methods for detecting, isolating and purifying immunoglobulins and immunoglobulin fragments using the immobilized Protein G variants of the invention.

Surprisingly, it has been discovered that the immobilized Protein G variants of the invention exhibit binding characteristics with immunoglobulin and immunoglobulin fragments which are unlike those of Protein G. Therefore, the immobilized Protein G variants of the invention can be used in new and unexpected ways to effect the detection, isolation and purification of immunoglobulins and immunoglobulin fragments. They may also have a high binding capacity for Ig or fragments thereof.

The present invention provides cloned genes encoding Protein G variants. By the term "Protein G variant" is intended proteins comprising one or more natural IgG binding domains of Protein G, hybrids of the natural IgG binding domains, and mutants thereof wherein the variant retains the capability of binding Ig, or fragments thereof (the term "variant" may be taken to exclude naturally occurring Protein G). Thus a "variant" can be thought of as a protein differing from naturally occurring Protein G by the deletion, addition or substitution of one or more amino acid residues so as not to substantially alter the sequence or properties thereof.

By the term "hybrid sequence" is intended DNA or amino acid sequences which contain portions of the respective sequences corresponding to B1 and B2 and which retain immunoglobulin binding properties. Such a hybrid sequence is shown in Figure 9 and is labeled B3. This hybrid sequence comprises the first 6 amino acids of the binding domain B2 fused to the last 49 amino acids of the B1 domain. Thus, it is intended that all such hybrid sequences which retain immunoglobulin binding properties are within the scope of this invention.

Methods for obtaining such Protein G variants are described in detail in the Examples, below. One of ordinary skill in the art can screen such Protein G variants for the capability of binding Ig or fragments thereof with no more than routine screening. For example, the Protein G variant may be contacted with Ig or a fragment thereof followed by detection of binding between the Protein G variant and Ig or fragment thereof. Methods for the detection of binding between two proteins are well known to those of ordinary skill in the art.

Protein G genes may be derived from the Protein G gene of the *Streptococcus Sp.*, Lancefield Group G strain or from strain G148. The invention also provides for Protein G genes inserted into a cloning vector. Cells of a prokaryotic organism which have been stably transformed with recombinant vectors are disclosed.

The invention further provides the identification of the nucleotide sequence and amino acid sequence for the active binding sites of the Protein G molecule. Also provided are eleven genes encoding single domain Protein G variants. The Protein G variants expressed therefrom, when immobilized on a solid phase support, exhibit altered Ig binding specificities unlike those of Protein G. Protein G variants do not contain the lethal sequences which naturally flank the protein G gene and which limit the quantity of protein G which may be expressed by a recombinant host.

Cloning of the Protein G gene and production of Protein G and Protein G variants in bacterial hosts, such as *E. coli* or *Bacillus subtilis*, through recombinant DNA technology, according to the methods of the present invention, provides a number of advantages over current methods for obtaining the protein. By the methods of this invention, relatively high production levels of microbial Protein G and protein G variants can be obtained. Moreover, the proteins can be produced under conditions where they can be isolated more favorably, and the proteins can be produced in a non-pathogenic host. The cloned genes may be inserted into various multicopy expression vectors to give enhanced levels of these valuable IgG-binding proteins in cultured *E. coli* cells transformed with the recombinant expression vectors. Production of Protein G and Protein G variants in *E. coli* or *B. subtilis* cells is preferable to cultivation of Protein G-producing Streptococcal strains, which are commonly pathogenic strains.

The first step in the cloning of the Protein G gene, according to the present invention, is isolation of Streptococcal strains that produce Protein G. This may be done by assaying various strains for IgG binding activity using any suitable immunoassay technique. A technique used by the Applicant is the colony

immunoassay described in detail in the examples section below. Strains found to have IgG-binding activity are next tested for the ability to bind IgG3 as well as unfractionated IgG, since the ability to bind IgG3 is a desired property associated with Protein G. A hemagglutination assay using red blood cells coated either with IgG3 or with unfractionated IgG (described in detail in the examples below) is a convenient method for identifying Protein G-producing strains. A known Protein A-producing strain, such as *Staphylococcus aureus* Cowan I [Sjoquist, J., *Eur. J. Biochem.*, 78 : 471-490 (1977)], may be used as a control, since Protein A binds unfractionated IgG but not IgG3.

Chromosomal DNA is isolated from strains found to produce Protein G by cultivating the strains in a nutrient medium to a desired cell density, then lysing the cells by any of the conventional chemical, mechanical, and/or enzymatic methods known in the art. Conventional extraction and precipitation procedures are used to isolate the chromosomal DNA. Fragments of DNA of a suitable size for cloning are obtained by such known mechanical methods as sonication or high-speed stirring in a blender, or by enzymatic methods, such as partial digestion with DNaseI, which gives random fragments, or with restriction endonucleases, which cleave at specific sites.

The chromosomal DNA fragments then are inserted into a cloning vector. Any suitable plasmid or bacteriophage cloning vector may be used. For a vector to be suitable, it should have several useful properties. It should have an origin of replication that is functional in the intended microbial host cells, and a selectable marker (such as an antibiotic resistance gene) to aid in identification of host cells that have been transformed with the vector. It should be able to accept inserted DNA fragments and still replicate normally. Preferably, the vector comprises one or more unique restriction endonuclease recognition sites at which DNA fragments can be inserted without destroying the vector's ability to replicate.

Suitable cloning vectors include phage derivatives such as lambda gtl [Young and Davis, *Proc. Nat'l Acad. Sci. U.S.A.*, 80 :1194-1198 (1983)], the various phage M13-derived vectors such as M13mp9 (commercially available from Bethesda Research Laboratories), plasmids such as pBR322, and many others [Old and Primrose, *Principles of Gene Manipulation*, 2nd. Ed., Univ. of Calif. Press, pgs. 32-35 and 46-47 (1981)]. The Applicant used a pBR322-derived plasmid vector pGX1066, shown in Figure 1.

The Streptococcal DNA is inserted into the cloning vector by such methods as homopolymeric tailing or by using linker molecules (Old and Primrose, *supra* at page 92). Advantageously, the vector is linearized with a restriction endonuclease, and the chromosomal DNA is also digested with a restriction endonuclease that produces DNA fragments that are ligatable to the ends of the linearized vector molecule. The Streptococcus-derived DNA fragments are thus advantageously inserted into the cloning vector in a standard reaction using the enzyme T4 DNA ligase.

Bacterial cells are transformed with the recombinant cloning vector, using standard procedures, and the bacterial colonies are screened for production of Protein G. Assays such as the colony immunoassay and the hemagglutination assay described in the examples below are suitable for identification of recombinant strains producing Protein G. As described more fully in Example I below, the initial positive colony identified was unstable. Through purification procedures in which this clone underwent several rounds of restreaking, a derivative of the clone was obtained which appeared stable and produced Protein G. This strain was designated *E. coli* GX7820.

Plasmid DNA from this strain was isolated and then analyzed by restriction analysis followed by gel electrophoresis. It has been determined that the strain contains two plasmids. One, designated pGX1066X, appears to be approximately the same size as the pGX1066 cloning vector; the other, designated pGX4530, appears to be pGX1066 containing an 11 kilobase-pair (kbp) insert. Although the Applicant does not wish to be bound by a particular theory, it appears, as illustrated more fully in the examples, that pGX1066X is a "cryptic helper plasmid", a derivative of pGX1066 in which the ampicillin resistance gene is no longer intact. The original transformant strain probably contained pGX1066 and pGX4530, and was unstable because pGX4530 was lost from the cells due to lack of selective pressure to retain that plasmid when pGX1066 was present to provide ampicillin resistance. Once pGX1066X appeared, having a mutation that inactivated its ampicillin resistance gene, only those host cells which had retained pGX4530 (having an intact ampicillin resistance gene) could survive on the ampicillin plates. Plasmid pGX1066X is retained in the cells containing both plasmids, presumably because it serves to limit the copy number of pGX4530 in the cell. Plasmid pGX4530 alone is lethal to the host cells (see Example 1) since it has DNA sequences which are lethal to the host. However, the presence of pGX1066X in the same host cell reduces the copy number of pGX4530 to a tolerable level. The plasmids are from the same "incompatibility group", i.e., the plasmids compete with each other for maintenance in the cell, so that each plasmid limits the copy number of the other in the host cell. *E. coli* strain GX7820 has been deposited with the American Type Culture Collection in Rockville, Maryland, and given accession number 53460.

An *E. coli* strain was transformed with a mixture of the plasmids isolated from strain GX7820. The

transformation resulted in a number of tiny, strongly positive colonies with a few (about 20%) resembling GX7820. From these tiny positive colonies have been isolated two stable variants which do not carry the helper plasmid and which are more strongly positive for Protein G than the original GX7820. One strain, designated GX7823, carries a plasmid (pGX4533) from which has been deleted a two kilobase pair (kbp) fragment of the insert in the pGX4530 plasmid. *E. coli* strain GX7823 has been deposited with the American Type Culture Collection in Rockville, Maryland and given accession number 53461. The other, designated GX7822, carries a plasmid which has acquired a three kbp insert of DNA within the original insert at a site very close to one end of the deletion in the plasmid carried by the GX7823 strain. The Protein G gene has been located on a 1.9 kilobase pair (kbp) fragment of the Streptococcal DNA insert on pGX4533.

To improve Protein G production levels, the cloned Protein G gene may be inserted into a variety of expression vectors. The expression vectors comprise "regulatory regions", which include DNA sequences necessary for gene expression, i.e., the transcription of DNA into mRNA followed by translation of the mRNA into the protein that the gene encodes. The Protein G gene may contain its natural expression signals, or those signals may be removed and the structural portion of the cloned Protein G gene (i.e., the protein-encoding portion of the gene) can be operably fused, in accordance with conventional methods, to other expression signals, contained in an expression vector, which are capable of directing the Protein G gene in the chosen host organism. For example, when the host microorganism is *E. coli*, the expression vector may comprise such known regulatory regions as the *trp* promoter/operator, the *lac* promoter/operator, the bacteriophage lambda *P_L* promoter/operator, and many others.

In one embodiment of the invention, the expression vector further comprises a DNA sequence homologous to a region of the chromosome of the host microorganism. This construction permits linear integration of the vector into the host chromosome in the region of homology. An advantage to this method is that there is less likelihood of loss of the Protein G sequence from the host, due to negative selection favoring vector-free cells.

Protein G may be produced at high levels in bacterial cells transformed with such recombinant expression vectors. In addition, production of Protein G within the cell may be controlled by using promoter/operator systems which may be induced (to begin gene expression) at a desired cell density, or in which gene expression can be reversibly repressed until the cell density in a culture of recombinant bacterial cells has reached a desired level. The potentially negative effects on cell growth of production of a heterologous protein can thus be avoided.

Transformed cells containing a cloned Protein G or a Protein G variant gene are cultivated under protein-producing conditions such that Protein G or a Protein G variant is produced by the cells. Cultivation conditions, including large-scale fermentation procedures, are well known in the art. The cells may be cultivated under any physiologically-compatible conditions of pH and temperature, in any suitable nutrient medium containing assimilable sources of carbon, nitrogen and essential minerals that supports cell growth. Protein-producing cultivation conditions will vary according to the type of vector used to transform the host cells. For example, certain expression vectors comprise regulatory regions which require cell growth at certain temperatures, or addition of certain chemicals to the cell growth medium, to initiate the gene expression which results in production of Protein G or a Protein G variant. Thus, the term "protein producing conditions" as used herein is not meant to be limited to any one set of cultivation conditions.

Advantageously, the cloned gene is transferred to *B. subtilis* by methods previously applied to the gene encoding Protein A and described in commonly assigned United States Patent No. 4,617,266 (1986), incorporated herein by reference in its entirety. In accordance with these methods, Protein G can be synthesized in *B. subtilis*.

The functionally active portions of Protein G was localized to a repeating structure by examining the IgG-binding activity of protein produced by *E. coli* strains carrying modified forms of the cloned protein G gene. In a preferred embodiment, the invention also relates to a cloned gene which encodes one or more of the Ig binding portions of Protein G (Protein G variants) and to the protein so produced which has immunoglobulin binding properties. The details of the identification and isolation of the gene coding for the active binding sites of Protein G are set forth in Example III below. The DNA sequences, and the amino acid sequences encoded thereby, of two genes encoding, respectively, two and three active sites per Protein G molecule are set forth in Figures 8 and 9. With this information, it is now possible to produce Protein G variants which contain one or more Protein G binding sites. Synthetic genes may be constructed, utilizing known synthetic procedures, which code for from one to twenty or more active sites within a given amino acid sequence, thereby providing higher binding efficiency, capacity, and specificity to the resulting material. A preferred Protein G variant contains 1 to 10 active binding sites; a more preferred material contains one active binding site.

Also within the scope of this invention are Protein G variants having immunoglobulin-binding properties

which, further have deletions or substitutions of amino acids or additional amino acids at the amino or carboxyl terminus thereof.

Preferred forms of the Protein G variants are encoded by genes from which coding sequences upstream and downstream from the active sites (B1 and B2) have been deleted. The details regarding the deletion of such coding sequences are set forth in the Examples, below.

In a preferred embodiment, a cloned gene encoding Protein G variant which encodes a protein comprising the B1 and B2 domains (Type 1), which may be used in the practice of the invention, has the following DNA sequence:

```

10      10      20      30      40      50      60
    ATGGATCCTG CATTACCTAA GACTGACACT TACAAATTAA TCCTTAATGG TAAACATTG
    AAAGGCGAAA CAACTACTGA AGCTGTTGAT GCTGCTACTG CAGAAAAAGT CTTCAACAA
    TACGCTAACG ACAACGGTGT TGACGGTGAA TGGACTTACG ACGATGCGAC TAGACCTTT
    ACAGTTACTG AAAAACCAGA AGTGATCGAT GCGTCTGAAT TAACACCAGC CGTGACAACT
    TACAAACTTG TTATTAATGG TAAACATTG AAAGGCGAAA CAACTACTAA AGCAGTAGAC

15      310     320     330     340     350     360
    GCAGAACTG CAGAAAAAGC CTTCAACAA TACGCTAACG ACAACGGTGT TGATGGTGT
    TGGACTTATG ATGATGCGAC TAGACCTTT ACGGTAACG AAATGGTTAC AGAGGTTCCG
    BTCGCTTCAA AACBTAAAGA AGACTAA

```

or a degenerate variant thereof.

The Protein G variant Type 1 expressed from the above disclosed sequence has the following amino acid sequence:

```

25      5      10      15      20      25      30
    1 M D P A L P K T D T Y K L I L N G K T L K G E T T T E A V D
    31 A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T F
    61 T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T L
    91 K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G V
    121 W T Y D D A T K T F T V T E M V T E V P V A S K R K E D .

```

A second cloned gene encoding a Protein G variant which comprises the B1 and B2 binding domains (Type 2), which may be used in the practice of the invention, has the following DNA sequence:

```

35      10      20      30      40      50      60
    ATGGATCCGT ACCCATTACC TAAGACTGAC ACTTACAAAT TAATCCTTAA TGGTAAACA
    TTGAAGGCG AAACAACACTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGTCTTCAA
    CAATACGCTA ACGACAACGG TGTGACGGT GAATGGACTT ACGACGATGC GACTAAGACC
    TTTACAGTTA CTGAAAAACC AGAAGTGATC GATGCGTCTG AATTAACACC AGCCGAGACA
    ACTTACAACC TTGTTATTAA TGGTAAACA TTGAAGGCG AAACAACACTAC TAAGCAGTA

40      310     320     330     340     350     360
    GACGAGAAA CTGCAGAAAA AGCCTTCAA CAATACGCTA ACGACAACGG TGTGATGGT
    GTTGGACTT ATGATGATGC GACTAAGACC TTTACGGTAA CTGAAATGGT TACAGAGTT
    CCTCGAGGTG ATGCACCAAC TGAACCAGAA AAACCAGAAG CAAGTATCCC TCTTGTCCG
    TTAACCTCTG CAACTCCAAT TGCTAAGAT GACGCTAAGA AAGACGATAC TAAGAAAGAA
    BATGCTAAAA AACCAGAAGC TAAGAAAGAT GACGCTAAGA AAGCTGAAC TGCCGGCTAA

45

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or a degenerate variant thereof.

The Protein G variant Type 2 expressed from the second cloned gene having the above disclosed sequence has the following amino acid sequence:

```

50      5      10      15      20      25      30
    1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
    31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
    61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
    91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
    121 V W T Y D D A T K T F T V T E M V T E V P R G D A P T E P E
    151 K P E A S I P L V P L T P A T P I A K D D A K K D D T K K E
    181 D A K K P E A K K D D A K K A E T A G .

```

A third cloned gene encoding a Protein G variant comprising the B1 and B2 binding domains (Type 3), which may be used in the practice of the invention, has the following DNA sequence:

```

5      10      20      30      40      50      60
ATGGATCCGT ACCCATTACC TAAGACTGAC ACTTACAAAT TAATCCTTAA TGGTAAACAA
TTGAAAGGCG AAACAACCTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGTCTTCAAA
CAATACGCTA ACGACAACGG TGTGACGGT GAATGGACTT ACGACGATGC GACTAAGACC
TTTACAGTTA CTGAAAAACC AGAAGTGATC GATGCGTCTG AATTAACACC AGCCGTGACA
ACTTACAAAC TTGTTATTAA TGGTAAACAA TTGAAAGGCG AAACAACCTAC TAAAGCAGTA

10      310      320      330      340      350      360
GACGCAGAAA CTGCAGAAAA AGCCTTCAAA CAATACGCTA ACGACAACGG TGTGATGGT
GTTTGACTT ATGATGATGC BACTAAGACC TTTACGGTAA CTGAAATGST TACAGAGGTT
CCTCGATCGT GCTAA

```

or a degenerate variant thereof.

The Protein G variant Type 3 expressed from the third cloned gene having the above disclosed sequence has the following amino acid sequence:

```

20      5      10      15      20      25      30
1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
121 V W T Y D D A T K T F T V T E M V T E V P R S C.

```

A fourth cloned gene encoding a Protein G variant comprising the B1 and B2 domains (Type 4), which may be used in the practice of the invention, has the following DNA sequence:

```

30      10      20      30      40      50      60
GTGAGAGGCA AAAAAGTATG GATCAGTTTG CTGTTTGCTT TAGCGTTAAT CTTTACGATT
GCGTTCCGCA GCACATCCTC TGCCCAGGCG GCAGGGGATC CAATCGAAGA TACCCCAATT
ATTCGTAATG GTGGTGAATT AACTAATCTT CTGGGGAATT CAGAGACAAC ACTGGCTTTG
CGTAATGAAG AGAGTGCTAC AGCTGGGTAC CCATTACCTA AGACTGACAC TTACAAATTA
ATCCTTAATG GTAAACATT GAAAGGCGAA ACACTACTG AAGCTGTTGA TGCTGCTACT

35      310      320      330      340      350      360
GCAGAAAAAG TCTTCAACAA ATACGCTAAC GACAACGGTG TTGACGGTGA ATGGACTTAC
GACGATGCGA CTAAGACCTT TACAGTTACT GAAAAACCA GAAATGATCGA TGCCTCTGAF
TTAACACCA GCGTGACAAC TTACAAACTT GTTATTARTG GTAAACATT GAAAGGCGAA
ACAACTACTA AAGCAGTAGA CGCAGAACT GCAGAAAAAG CCTTCAACAA ATACGCTAAC
GACAACGGTG TTGATGGTGT TTGACTTAT GATGATGCGA CTAAGACCTT TACGGTAACT

40      610      620      630      640      650      660
GAAATGGTTA CAGAGGTTCC TCGAGGTGAT GCACCAACTG AACCAGAAAA ACCAGAGCA
AGTATCCCTC TTGTTCCGTT AACTCCTGCA ACTCCARTG CTAAGATGA CGCTAAGAAA
BACGATACTA AGAAGAGAGA TGCTAAAAAA CCAGAGGCTA AGAAGATGA CGCTAAGAAA
GCTGAAACTG CCGGCTAA

```

or a degenerate variant thereof.

The Protein G variant Type 4 expressed from the fourth cloned gene having the above disclosed sequence has the following amino acid sequence (without the 30 amino acid secretion sequence):

```

50      5      10      15      20      25      30
1 A G D P I E D T P I I R N G G E L T N L L G N S E T T L A L
31 R N E E S A T A G Y P L P K T D T Y K L I L N G K T L K G E
61 T T T E A V D A A T A E K V F K Q Y A N D N G V D G E W T Y
91 D D A T K T F T V T E K P E V I D A S E L T P A V T T Y K L
121 V I N G K T L K G E T T T K A V D A E T A E K A F K Q Y A N
151 D N B V D G V W T Y D D A T K T F T V T E M V T E V P R S D
181 A P T E P E K P E A S I P L V P L T P A T P I A K D D A K K
55 211 D D T K K E D A K K P E A K K D D A K K A E T A G.

```

A fifth cloned gene encoding a Protein G variant which comprises the single binding domain B2 (Type

5), which may be used in the practice of the invention, has the following DNA sequence:

```

      10      20      30      40      50      60
5  ATGGATCCAG GCGATGCGTC TGAATTAACA CCAGCCGTGA CAACTTACAA ACTTGTATT
   AATGGTAAAA CATTGAAGG CGAAACAAC ACTAAAGCAG TAGACGCAGA AACTGCAGAA
   AAAGCCTTCA AACAATACGC TAACGACAAC GGTGTTGATG GTGTTTGGAC TTATGATGAT
   GCGACTAAGA CCTTTACGGT AACTGAAATG GTTACAGAGG TTCCTCGAGG TGATGCACCA
   ACTGAACCAG AAAAACCAGA AGCAAGTATC CCTCTTGTTT CGTAACTCC TGCAACTCCA

      310      320      330      340      350      360
10 ATTGCTAAAG ATGACGCTAA GAAAGACBAC ACTAAGAAAG AAGATGCTAA AAAACCAGAA
   SCTAAGAAAG ATGACGCTAA GAAAGCTGAA ACTGCCGGCT AA

```

or a degenerate variant thereof.

15 The Protein G variant Type 5 expressed from the fifth cloned gene having the above disclosed sequence has the following amino acid sequence:

```

      5      10      15      20      25      30
20  1 M D P G D A S E L T P A V T T Y K L V I N G K T L K G E T T
   31 T K A V D A E T A E K A F K Q Y A N D N G V D G V W T Y D D
   61 A T K T F T V T E M V T E V P R G D A P T E P E K P E A S I
   91 P L V P L T P A T P I A K D D A K K D D T K K E D A K K P E
  121 A K K D D A K K A E T A G.

```

25 A sixth cloned gene encoding a Protein G variant comprising the B1, B1/B2 hybrid domain and B2 domain (Type 6), which may be used in the practice of the invention, has the following DNA sequence:

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      10      20      30      40      50      60
30  ATGGATCCGT ACCCATTACC TAAGACTGAC ACTTACAART TAATCCTTAA TGGTAAACAA
   TTGAAGGGCG AAACAACACTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGTCTTCAAA
   CAATACGCTA ACGACAACGG TGTTGACGGT GAATGGACTT ACGACGATGC GACTAAGACC
   TTTACAGTTA CTGAAAAACC AGAAGTGATC GATGCGTCTG AATTAAACACC AGCCGTGACA
   ACTTACAAC TTGTTATTAA TGGTAAACAA TTGAAGGGCG AAACAACACTAC TAAAGCAGTA
      310      320      330      340      350      360
   GACGCAGAAA CTGCAGAAAA AGTCTTCAAA CAATACGCTA ACGACAACGG TGTTGACGGT
   GAATGGACTT ACGACGATGC GACTAAGACC TTTACAGTTA CTGAAAAACC AGAAGTGATC
   GATGCGTCTG AATTAAACACC AGCCGTGACA ACTTACAAC TTGTTATTAA TGGTAAACAA
35  TTGAAGGGCG AAACAACACTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGCCTTCAAA
   CAATACGCTA ACGACAACGG TGTTGATGGT GTTTGGACTT ATGATGATGC GACTAAGACC
      610      620      630      640      650      660
   TTTACGGTAA CTGAAATGGT TACAGAGGTT CCTCGAGGTG ATGCACCAAC TGAACCAGAA
   AAACCAAGAA CAAGTATCCC TCTTGTTCCG TTAACCTCTG CAACTCCCAT TGCTAAGAT
   GACGCTAAGA AAGACGATAC TAAGAAAGAA GATGCTAAAA AACCAGAGGC TAAGAAAGAT
40  GACGCTAAGA AAGCTGAAAC TGCCGCTAA

```

or a degenerate variant thereof.

45 The Protein G variant Type 6 expressed from the sixth cloned gene having the above disclosed sequence has the following amino acid sequence:

```

      5      10      15      20      25      30
50  1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
   31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
   61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
   91 L K G E T T T E A V D A A T A E K V F K Q Y A N D N G V D G
  121 E W T Y D D A T K T F T V T E K P E V I D A S E L T P A V T
   151 T Y K L V I N G K T L K G E T T T K A V D A E T A E K A F K
   181 Q Y A N D N G V D G V W T Y D D A T K T F T V T E M V T E V
   211 P R G D A P T E P E K P E A S I P L V P L T P A T P I A K D
55  241 D A K K D D T K K E D A K K P E A K K D D A K K A E T A G.

```

A seventh cloned gene encoding a Protein G variant comprising the single B2 binding domain (Type 7), which may be used in the practice of the invention, has the following DNA sequence:

5

or a degenerate variant thereof.

The Protein G variant Type 7 expressed from the seventh cloned gene having the above disclosed sequence, has the following amino acid sequence:

```

      5      10      15      20      25      30
1  M D P G D A S E L T P A V T T Y K L V I N G K T L K G E T T
31 T K A V D A E T A E K A P K Q Y A N D N G V D G V W T Y D D
61 A T K T F T V T E M V T E V P V A S K R K E D ,

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15

An eighth cloned gene encoding a Protein G variant comprising the binding domains B1 and B2 (Type 8), which may be used in the practice of the invention, has the following DNA sequence:

20

```

      10      20      30      40      50      60
1  ATGGATCCGT ACCCATTACC TAAGACTGAC ACTTACAAAT TAATCCTTAA TGGTAAAACA
61 TTGAAAGGCG AAACAACCTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGTCTTCAAA
121 CAATACGCTA ACGACAACGG TGTGACGGT GAATGGACTT ACGACGATGC GACTAAGACC
181 TTTACAGTTA CTGAAAAACC AGAAGTGATC GATGCGTCTG AATTAAACACC AGCCGTGACA
241 ACTTACAAAC TTGTTATTAA TGGTAAAACA TTGAAAGGCG AAACAACCTAC TAAAGCAGTA

      310      320      330      340      350      360
301 GACGCAGAAA CTGCAGAAAA AGCCTTCAAA CAATACGCTA ACGACAACGG TGTGATGGT
361 GTTTGGACTT ATGATGATGC GACTAAGACC TTTACGGTAA CTGAAATGGT TACAGAGGTT
421 CCTCGAGGTG ATGCACCAAC TGAACCAGAA AAACCAGAAAG CAAGTATCCC TCTTGTCCG
481 TTAACCTCTG CAACTCCAAT TGCTAAAGAT GACGCTAAGA AAGACGATAC TAAGAAAGAA
541 GATGCTAAAA AACCAGAAGC TAAGAAAGAT GACGCTAAGA AAGCTGAAC TGCCCTTCA

```

25

30

601 TGCTAA

35

or a degenerate variant thereof.

The Protein G variant Type 8 expressed from the eighth cloned gene having the above disclosed sequence, has the following amino acid sequence:

```

      5      10      15      20      25      30
1  M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
121 V W T Y D D A T K T F T V T E M V T E V P R G D A P T E P E
151 K P E A S I P L V P L T P A T P I A K D D A K K D D T K K E
181 D A K K P E A K K D D A K K A E T A P S C .

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40

45

A ninth cloned gene encoding a Protein G variant comprising the B1 and B2 binding domains (Type 9), which may be used in then practice of the invention, has the following DNA sequence:

50

55

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10 20 30 40 50 60
 1 ATGGATCCGT ACCCATTACC TAAGACTGAC ACTTACAAAT TAATCCTTAA TGGTAAACAA
 61 TTGAAAGGCG AAACAACCTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGTCTTCAAA
 121 CAATACGCTA ACGACAACGG TGTGACGGT GAATGGACTT ACGACGATGC GACTAAGACC
 181 TTTACAGTTA CTGAAAAACC AGAAGTGATC GATGCGTCTG AATTAACACC AGCCGTGACA
 241 ACTTACAAAC TTGTTATTAA TGGTAAACAA TTGAAAGGCG AAACAACCTAC TAAAGCAGTA
 310 320 330 340 350 360
 301 GACGCAGAAA CTGCAGAAAA AGCCTTCAAA CAATACGCTA ACGACAACGG TGTGATGGT
 361 GTTGGACTT ATGATGATGC GACTAAGACC TTTACGGTAA CTGAAATGGT TACAGAGGTT
 421 CCTCGAGGTG ATGCACCAAC TGAACCAGAA AAACCAGAG CAGGTATCCC TCTTGTCCG
 481 TTAACAGCT GCTAA

or a degenerate variant thereof.

The Protein G variant Type 9 expressed from the ninth cloned gene having the above disclosed sequence, has the following amino acid sequence:

5 10 15 20 25 30
 1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
 61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
 91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
 121 V W T Y D D A T K T F T V T E M V T E V P R G D A P T E P E
 151 K P E A S I P L V P L T S C.

A tenth cloned gene encoding a Protein G variant comprising the single B1 binding domain (Type 10), which may be used in the practice of the invention, has the following DNA sequence:

10 20 30 40 50 60
 ATGGATCCGT ACCCATTACC TAAGACTGAC ACTTACAAAT TAATCCTTAA TGGTAAACAA
 TTGAAAGGCG AAACAACCTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGTCTTCAAA
 CAATACGCTA ACGACAACGG TGTGACGGT GAATGGACTT ACGACGATGC GACTAAGACC
 TTTACAGTTA CTGAAAAACC AGAAGTGATC GATGCGTCTG AATTAACACC AGCCGTGACA
 CCAGAAAAAC CAGAAACAAG TATCCCTCTT GTTCCGTTAA CTCCTGCAAC TCCAATTGCT
 310 320 330 340 350 360
 AAAGATGACG CTAAGAAAGA CGATACTAAG AAAGAAGATG CTAAGAAACC AGAAGCTAAG
 AAAGATGACG CTAAGAAAGC TGAAGCTGCC GGCTAA

or a degenerate variant thereof.

The Protein G variant Type 10 expressed from the tenth cloned gene having the above disclosed sequence, has the following amino acid sequence:

5 10 15 20 25 30
 1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
 61 F T V T E K P E V I D V P R G D A P T E P E K P E A S I P L
 91 V P L T P A T P I A K D D A K K D D T K K E D A K K P E A K
 121 K D D A K K A E T A G.

An eleventh cloned gene encoding a Protein G variant comprising a B1'/B2 hybrid binding domain (Type 11), which may be used in the practice of the invention, has the following DNA sequence:

```

      10      20      30      40      50      60
ATGGATCCGT ACCATTACC TAAGACTGAC ACTTACAAAT TAATCCTTAA TGGTAAACA
TTGAAAGGCG AACAACACTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGCCTTCAAA
CAATACGCTA ACGACAACGG TGTGATGTT GTTGGACTT ATGATGATGC GACTAAGACC
5 TTTACGGTAA CTGAAATGGT TACAGAGGTT CCTCGAGGTG ATGCACCAAC TGAACCAGAA
AAACCAGAAG CAAGTATCCC TCTTGTCCG TTAACCTCTG CAACTCCAAT TGCTAAAGAT

      310      320      330      340      350      360
GACGCTAAGA AAGACGATAC TAAGAAAGAA GATGCTAAAA AACCAGAAGC TAAGAAAGAT
GACGCTAAGA AAGCTGAAC TGCCGGCTAA

```

or a degenerate variant thereof.

The Protein G variant Type 11 expressed from the eleventh cloned gene having the above disclosed sequence, has the following amino acid sequence:

```

      5      10      15      20      25      30
1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T E A V
31 D A A T A E K A F K Q Y A N D N G V D G V W T Y D D A T K T
61 F T V T E M V T E V P R G D A P T E P E K P E A S I P L V P
91 L T P A T P I A K D D A K K D D T K K E D A K K P E A K K D
121 D A K K A E T A G.

```

By the terms "degenerate variant" is intended DNA sequences having substitutions of bases but which encode the same protein.

It will be recognized by one skilled in the art that additional deletions and structural modifications of the Protein G variant genes can be constructed by analogous methods. It will further be recognized that various upstream deletions and various downstream deletions can be recombined in vitro in different combinations to produce novel gene structures. Such recombination can be facilitated by the use of unique restriction endonuclease sites for Sma I (upstream from the apr promoter), Kpn I (immediately upstream from sequences encoding domain B1) and Hind III (downstream from the coding sequences), by assorting Sma I-Kpn I fragments and Kpn I-Hind III fragments. Novel combinations constructed in this way retain sequences encoding the B domains, and therefore retain IgG-binding activity. Additionally, it will be recognized that the Sma I-Bam HI fragment of these plasmids which carries the apr promoter and signal-encoding sequences can be replaced by analogous fragments carrying other promoters and signal-encoding sequences that are active in promoting synthesis and secretion of foreign proteins in B. subtilis.

Any suitable known method of protein purification may be used to recover and purify the Protein G variants from the host cells. The cells may be lysed, if necessary, using known chemical, physical, and/or enzymatic means. The Protein G then may be purified from the cell lysate using such standard procedures as adsorption to immobilized immunoglobulin, as described by Sjoquist, U.S. Patent No. 3,850,798 (1974), ion-exchange or gel chromatography, precipitation (e.g., with ammonium sulfate), dialysis, filtration, or a combination of these methods.

By the term "solid phase support" is intended any support capable of immobilizing the Protein G variants of the invention, either covalently, or by adsorption. Solid phase supports which may be used for immobilizing the Protein G variants of the invention include, but are not limited to, polymers having hydroxyl groups, either free or in esterified form, such as agarose, cellulose, including cellulose esters such as cellulose nitrate, diazocellulose, cellulose acetate, cellulose propionate, and the like, and acrylamide polymers and copolymers, such as polyacrylamide and acrylamide, microtitre plates, glass, polystyrene, polypropylene, polyethylene, dextran, nylon, agar, starch, or the chemically active membrane having a large surface area comprising a hydrophobic, microporous, skinless, polyamide membrane which is chemically bound to a residue of an activating agent which is capable of immobilizing the Protein G variants of the invention. See Degen et al., U.S. Patent No. 4,693,985 (1987).

The Protein G variants may be immobilized to the solid phase support according to methods known to those of ordinary skill in the art for protein immobilization. For example, the Protein G variants may be coated or bonded, either covalently or by adsorption, to the solid phase. Methods for immobilizing proteins to solid phase supports are taught, for example, in U.S. Patent Nos. 3,652,761, 3,879,262, 3,986,217, and 4,693,985. See also Examples XV and XVII of the present application. Preferably, the Protein G variants are immobilized to trisyl activated or cyanogen bromide activated agarose. Where the Protein G variant has one or more cysteine residues, a preferred method of immobilizing the Protein G variant is by coupling it to a maleimide-activated agarose support. This support may be prepared by treating agarose modified to

contain primary amino groups (in particular, AH-Sepharose, Pharmacia Co.) with sulfosuccinimidyl-4-(p-maleimidophenyl) butyrate. The resulting activated gel may then be treated with the Protein G variant to give the immobilized Protein G variant product. As disclosed in Example XVII, immobilization of cysteine containing variants using the maleimide-activated Sepharose derivative results in unexpectedly high levels of protein immobilization and unexpectedly high levels of Ig binding, especially with a mouse monoclonal antibody. Where the Protein G variant does not comprise a cysteine residue, the preferred method of immobilizing the Protein G variant is by coupling it to tressyl-activated agarose.

The immobilized Protein G variants of the invention may be used to separate or bind IgG or fragments thereof. Surprisingly, the inventors have discovered that certain immobilized Protein G variants exhibit unexpected binding profiles. In particular, it has been discovered that immobilized single domain variants bind to IgG and Fc fragments much better than to Fab and F(ab')₂ fragments. Therefore, these immobilized variants are useful for the separation of IgG and Fc fragments from Fab and F(ab')₂ fragments.

The immobilized single domain Protein G variants of the invention may be used in a method for the isolation of Fab or F(ab')₂ fragments from IgG and Fc fragments, comprising

- (a) contacting a sample comprising Fc fragments, IgG and at least one of Fab or F(ab')₂ fragments with a single domain Protein G variant immobilized on a solid phase support; and
- (b) washing the solid phase support obtained in step (a) with a buffer of pH 5 to 8 to give the Fab and F(ab')₂ fragments in the eluate and give a solid phase support with Fc fragments and IgG bound thereon.

Examples of buffers having pH 5 to 8 include, but are not limited to acetate, phosphate, Tris, borate, and bicarbonate.

The Fc fragment and IgG bound to the immobilized Protein G variant may then be recovered by (c) washing the solid phase support obtained in step (b) with a buffer of pH 3.5 to 2.4 to give the Fc fragment and IgG fragment in the eluate.

Examples of buffers having pH 3.5 to 2.4 include, but are not limited to acetate, citrate, and glycine.

In particular, the Type 5 Protein G variant, immobilized onto agarose, has little or no affinity for Fab or F(ab')₂ fragments but binds IgG and Fc fragments tightly and reversibly. IgG and Fc fragments are bound at about pH 5 to 8 while Fab and F(ab')₂ fragments are not bound. IgG and Fc fragments can be eluted by lowering the pH to about 3.5 to 2.4.

The inventors have also discovered that the single domain Protein G variant Type 10 immobilized to agarose binds IgG irreversibly (the IgG cannot be eluted by lowering the pH of the eluate), binds Fab and F(ab')₂ to a small extent at pH 5 to 8, and binds Fc. For example, at pH 5 to 8, Fc is bound but can be eluted by lowering the pH to 3.5 to 2.4.

The Immobilized Type 10 variant, having irreversibly bound and thus immobilized an IgG specific for any particular target molecule, may be used in affinity chromatography. In this embodiment of the invention, a target molecule bound to the target molecule specific IgG may be selectively eluted without elution of the IgG by washing the solid phase with a buffer of pH 3.5 to 2.4.

This aspect of the invention relates to a method for affinity chromatography of a target molecule, comprising

- (a) contacting a first sample comprising a target molecule-specific IgG with a solid phase support having Protein G variant Type 10 immobilized thereon to give IgG irreversibly immobilized to the solid phase support;
- (b) contacting a second sample comprising a target molecule with the solid support having the target molecule-specific IgG immobilized thereon obtained in step (a);
- (c) washing the solid phase support obtained in step (b) with a buffer of pH 5 to 8 to elute unbound solute; and
- (d) washing the solid phase support obtained in step (c) with a buffer of pH 3.5 to 2.4 to give the target molecule in the eluate.

The target molecule-specific IgG antibodies may be obtained according to methods known to those of ordinary skill in the art. Reference is made to Kohler *et al.*, *Nature* 256 :495 (1975) for methods of preparing antibodies.

The inventors have also discovered that the hybrid single domain Protein G Type 11 variant immobilized to agarose moderately binds IgG at pH 5 to 8, binds Fab to a smaller extent at pH 6 to 8, and binds Fc. For example, at pH 5 to 8, the Fc fragment is bound but may be eluted by lowering the pH to 3.5 to 2.4.

Unexpectedly, the inventors have discovered that the various subclasses of IgG including IgG1, IgG2, IgG3, and IgG4 may be fractionated and isolated using the Protein G variant Type 11 immobilized on a solid phase support.

In this embodiment, the invention relates to a method for fractionating the various subclasses of IgG, comprising

- (a) applying a sample comprising at least two subclasses of IgG to the top of a column containing the Protein G variant Type 11 immobilized to a solid phase support;
- (b) eluting the column with a buffer of pH 8 to 2.4 over a continuous or discontinuous gradient; and
- (c) collecting fractions of eluate containing the IgG subclasses.

5 The various IgG subclasses may be detected in the eluate by any means known to those of ordinary skill in the art. For example, the IgG subclasses may be detected with a commercially available isotyping kit (Amersham) or by ELISA or an immunodiffusion assay.

Examples of buffers which may be used in a gradient of pH 8 to 2.4 include, but are not limited to acetate, citrate, phosphate, Tris, glycine and borate.

10 The inventors have also discovered that cysteine-containing Protein G variants, when immobilized to maleimide activated agarose, provide high binding capacity for IgG and fragments thereof. This aspect of the invention relates to a method for the isolation of Fab or F(ab')₂ fragments from IgG and Fc fragments, comprising

- (a) contacting a sample comprising Fc fragments, IgG and at least one of Fab or F(ab')₂ fragments with a Protein G variant comprising at least one cysteine residue immobilized to maleimide activated agarose; and
- (b) washing the agarose obtained in step (a) with a buffer of pH 5 to 8 to give the Fab and F(ab')₂ fragments in the eluate and give agarose with Fc fragments and IgG bound thereon.

20 The invention also relates generally to methods for separating IgG from the impurities naturally associated therewith. This aspect of the invention relates to a method for the separation of IgG from impurities naturally associated therewith, comprising

- (a) contacting a sample comprising IgG with a Protein G variant immobilized to a solid phase support;
- (b) washing the solid phase support obtained in step (a) with a buffer of pH 5 to 8 to give the impurities in the eluate and IgG bound to the solid phase support; and
- (c) washing the solid phase support obtained in step (b) with a buffer of pH 3.5 to 2.4 to give IgG in the eluate which is free from the impurities naturally associated therewith.

The invention will now be described by way of example with reference to the following Examples and to the accompanying drawings, in which:

Figure 1 is a diagram showing the salient features of plasmid pGX1066, a vector suitable for use in cloning a Protein G-encoding DNA fragment;

Figure 2 shows a partial restriction map of plasmid pGX4533, a recombinant plasmid vector containing a Protein G-encoding DNA fragment;

Figures 3 and 3A-C shows a DNA sequence for the Protein G gene, as well as the amino acid sequence encoded by the gene;

Figure 4 shows the restriction map of the cloned protein G gene and the repeating structure of its protein product responsible for IgG-binding;

Figure 5 shows the partial restriction map of mGX4547, a bacteriophage vector containing a Protein G-encoding fragment;

Figure 6 shows the partial restriction map of mGX7880, a bacteriophage vector which contains two complete copies of the B structure and lacks all amino acid sequences distal to B1 and B2;

Figure 7 shows a restriction map of plasmid pGX4582, a recombinant plasmid vector used to transform *B. subtilis* which contains a Protein G-encoding fragment;

Figures 8 and 8A-C show the location of the active sites, B1 and B2, on Protein G as coded for by the cloned Protein G gene derived from streptococcus GX7809;

Figures 9 and 9A show the DNA and amino acid sequences for the cloned Protein G gene derived from streptococcus GX7805. This gene codes for a Protein G containing three active sites;

Figure 10 shows the relationship between the repeating structures of the Protein G gene derived from strains GX7805 and GX7809;

Figure 11 depicts construction of plasmid pGX4595 from plasmid pGX4582 wherein coding sequences upstream from the active sites sequences have been deleted;

Figure 12 depicts construction of plasmids pGX4597 and pGX4599 from plasmid mGX7872 wherein coding sequences downstream from the active sites have been deleted;

Figure 13 depicts the construction of plasmids pGX5203 (which expresses Protein G variant Type 3) and pGX5204 (which expresses Protein G variant Type 2) from plasmids pGX4597 and pGX4599 respectively and the plasmid pGX2606 which contains the promoter OL/PR;

Figure 14 depicts the construction of plasmid pGX4592 which contains the gene which encodes Protein G variant Type 1;

Figure 15 depicts the construction of plasmid pGX5245 which contains the gene which encodes Protein

G variant Type 5;

Figure 16 depicts the construction of plasmids pGX5247 and pGX5246 which contain genes which encode Protein G variants Type 6 and Type 11, respectively;

Figure 17 depicts the construction of plasmid pGX5244 which contains the gene which encodes Protein G variant Type 7;

Figure 18 depicts the construction of plasmids pGX5255 and pGX5268 which contain genes which encode Protein G variants Type 8 and Type 9, respectively;

Figure 19 depicts the construction of plasmid pGX5266 which contains the gene which encodes Protein G variant type 10.

The following Examples are provided to illustrate the invention, and are not to be construed as limiting the scope of the invention in any manner.

EXAMPLE I

Cloning a Streptococcus Protein G Gene into E. coli

Streptococci of Lancefield group G were obtained from hospitals, and 11 independent isolate strains were derived from the clinical isolates. Each strain was assayed for ability to bind IgG using the following colony immunoassay procedure. The strains were streaked on L-Broth-agar plates which had been overlaid with a sheet of nitrocellulose and (top layer) a sheet of cellulose acetate ("immunoassay plates"). The plates were incubated at 37° C until bacterial colonies were visible on the cellulose acetate sheet.

The nitrocellulose sheets then were removed from the plates, and IgG-binding proteins were detected on the sheets using an immunochemical procedure, as follows. The sheets were first treated with bovine serum albumin (3.0% w/v in "Tris-saline", which comprises 0.01M Tris-HCl, pH 8.0, and 0.15M NaCl) to block nitrocellulose sites to minimize non-specific binding of antibodies to the nitrocellulose in subsequent steps. The sheets then were treated with normal rabbit serum (diluted 1:1000 in Tris-saline containing 3% w/v bovine serum albumin) for 1 hour at 23° C, followed by peroxidase-conjugated goat anti-rabbit IgG (similarly diluted), and, finally, with 4-chloro-1-naphthol (0.6 mg/ml) and hydrogen peroxide (0.06% w/v in Tris-saline containing 0.2 volume methanol), washing the sheets with Tris-saline between incubation steps. Blue spots on the nitrocellulose sheet indicate the presence of IgG-binding protein, and the blue areas correspond to microbial colonies which produced the IgG-binding protein.

Nine of the strains were positive, i.e. were found to bind IgG, although to varying degrees. Several of the strains were next tested for ability to bind IgG3, using the following hemagglutination assay. Sheep red blood cells (RBC) (Cappel Laboratories, Malvern, Pennsylvania) were coated with immunoglobulin essentially as described by Adler and Adler [Meth. Enzymol. 70 :455-466 (1980)]. RBC were washed with phosphate-buffered saline (PBS, containing 8.4 g/l NaCl, 1.1g/l Na₂HPO₄, and 0.27 g/l NaH₂PO₄) and treated for 15 min. at 37° C with a solution of tannic acid at 2.5 mg/ml in PBS. Cells were recovered by centrifugation and resuspended in PBS containing, at 0.2 mg/ml, either (a) total human immunoglobulin G (available from Sigma Chemical Co; St. Louis, Mo.), (b) IgG3 myeloma protein or (c) PBS only. After incubation at 37° C for 30 min, RBC were recovered by centrifugation and washed with PBS. For the agglutination assay, 50 ul of a 1% suspension of coated RBC were mixed with 50 ul of a test cell extract, diluted serially in PBS, in a conical well of a multiwell dish. Unagglutinated RBC settle to the bottom of the well and form a small pellet, while agglutinated RBC form a more diffuse precipitate on the walls of the well.

Each of the positive group G Streptococcal strains agglutinated IgG3-coated erythrocytes as efficiently as erythrocytes coated with unfractionated IgG, which is expected for Protein G-producing strains. In contrast, *Staphylococcus aureus* Cowan I cells, a strain which produces Protein A, agglutinated red blood cells coated with unfractionated IgG, but showed no activity toward IgG3-coated cells, as expected. None of the cells agglutinated red blood cells which had been incubated with PBS only, i.e., uncoated red blood cells.

The same hemagglutination assay then was performed on supernatant fractions and cell extracts from cultures of the Streptococcus isolates and the isolates appeared to have differing localization of the IgG-binding activity. In some strains the activity appeared to be predominantly cell-bound, in some it was found predominantly in the culture supernatant, and some strains were intermediate. Three strains, which had differing localization of the IgG-binding activity, were chosen as sources of DNA for cloning the Protein G

gene.

Cells from each strain were cultivated in 250 mls. of Todd-Hewitt broth (commercially available from Fisher Scientific, Richmond, Va.) containing 20mM D,L-threonine. After 4 hours of cultivation, glycine was added to a final concentration in the culture medium of 5% (w/v). The cells were harvested by centrifugation after 5 hours of cultivation, when the cell density had reached an absorbance at 600nm of about 0.5 to 1.0. The cell pellets were washed with PBS and then frozen in liquid nitrogen and stored at -70°C. After thawing, the cells were washed with, and then resuspended in, 10 mls of S7 medium [described by Vasantha and Freese, *J. Bacteriology* 144 :1119-1125 (1980)] containing 0.5M sucrose, to which 200 ul of 5 mg/ml mutanolysin (commercially available from Sigma Chemical Co.) had been added. Following incubation at 37°C for 45 minutes, the resulting protoplasts were pelleted by centrifugation, and then lysed osmotically by resuspension in a solution containing 100mM EDTA, pH 8.0, 150mM NaCl, and 0.5 mg/ml Proteinase K. Following incubation at 37°C for 55 minutes, alpha-toluenesulfonyl fluoride (also called phenylmethanesulfonyl fluoride or PMSF, and available commercially, e.g. from Sigma) was added to a final concentration of 2mM, and the mixture was incubated at 70°C for 15 minutes to inactivate the Proteinase K. The cell lysate was extracted three times with chloroform/isoamyl alcohol (24:1) to further remove proteins, and an equal volume of isopropanol was added to the aqueous phase to precipitate the DNA. The precipitated DNA was collected by winding on a spool, and then was washed with 70% ethanol and dried in vacuo. The DNA pellets (from each of the 3 strains) were each resuspended in 0.5 ml of a 0.01M Tris-HCl (pH 7.8)/1mM EDTA/0.05 M NaCl solution. A portion of this isolated chromosomal DNA was partially digested with the restriction endonuclease Mbo I (commercially available) by adding 2 units of Mbo I to 25 ul of the resuspended DNA in 100 ul of a buffer containing 100 mM Tris-HCl, pH 7.8, 150 mM NaCl and 10mM MgCl₂. The reaction mixture was incubated at 37°C for 13 minutes, then at 70°C for 10 minutes. The digested DNA was subjected to electrophoresis on a 0.8% agarose gel for 15 hours at 0.35 volts/cm. The section of the gel containing DNA fragments between about 4 and 9 kilobase-pairs (kbp) in length was excised from the gel and crushed to aid in recovery of the DNA. An equal volume of H₂O-saturated phenol was added to the crushed gel portion, and the mixture was frozen at -70°C for 1 hour. Without prior thawing, the mixture was centrifuged at room temperature for 15 minutes in an Eppendorf microfuge, and the aqueous phase was extracted twice with an equal volume of phenol and once with an equal volume of phenol/chloroform/isoamyl alcohol (25:24:1). The DNA was precipitated from the aqueous phase by adding 2.5 volumes of 95% ethanol and 30 ug glycogen as a carrier.

The cloning vector into which the chromosomal DNA fragments were inserted was plasmid pGX1066, shown in Figure 1. This plasmid comprises a bank of closely-spaced restriction endonuclease recognition sites useful for insertion of DNA fragments to be cloned. The bank of cloning sites is bordered by two transcription terminators. *E. coli* strain GX1186, which constitutes strain GX1170 transformed by plasmid pGX1066 has been deposited with the ATCC as No. 39955. 3 ug of plasmid pGX1066 DNA were digested with the restriction endonuclease Bam HI (commercially available and used according to manufacturer's specifications.) The digested plasmid DNA then was treated with 1 unit calf intestine alkaline phosphatase, (obtained from Boehringer-Mannheim and used according to manufacturer's specifications) for 30 minutes at 37°C. Following extraction of the reaction mixture with phenol/chloroform/isoamyl alcohol (25:24:1), the DNA was precipitated by adding 0.1 volume 2M sodium acetate, 10mM EDTA, and 2.5 volumes 95% ethanol and 10 ug glycogen as a carrier. 0.5 ug of the pGX1066 vector DNA (Bam HI-digested and phosphatase-treated) then was ligated to 0.2 ug of the partially Mbo I digested *Streptococcus* chromosomal DNA prepared above. The 10 ul reaction mixture contained 1 unit of T4 DNA ligase (commercially available and used according to manufacturer's instructions) and was incubated at 4°C for 20 hours.

E. coli SK2267 (F⁻ gal⁺ thi⁺ T1⁺ hsdR4⁺ endA⁺ sbcB15⁺, available from the *E. coli* Genetic Stock Center, Yale University, New Haven, Conn.) cells were made competent for transformation by standard calcium chloride treatment, and 0.25 ml of the competent cells then were mixed with 20 ul of the ligation mixture in a standard transformation procedure [Lederberg and Cohen, *J. Bacteriol.* 119 :1072-1074 (1974)]. The cells then were pelleted by centrifugation and resuspended in 0.3 ml L Broth. 0.1 ml of cells then were plated on each of three L Broth-agar plates containing 100 ug/ml ampicillin, which had been overlaid with a sheet of nitrocellulose and (top layer) a sheet of cellulose acetate (immunoassay plates). The plates were incubated at 37°C until bacterial colonies were visible on the cellulose acetate sheet.

The nitrocellulose sheets then were removed from the plates, and IgG-binding proteins were detected on the sheets using the immunochemical procedure described above. The sheets were first treated with bovine serum albumin (3.0% w/v in tris-saline) to block nitrocellulose sites to minimize non-specific binding of antibodies to the nitrocellulose in subsequent steps. The sheets then were treated with normal rabbit serum, diluted 1:1000 in Tris-saline containing 3.0% w/v bovine serum albumin, for 1 hour at 23°C, followed by peroxidase-conjugated goat anti-rabbit IgG (diluted similarly), and, finally, with 4-chloro-1-naphthol (0.6

mg/ml) and hydrogen peroxide (0.06% w/v in Tris-saline containing 0.2 vol. methanol), washing with tris-saline between incubation steps.

One positive colony was identified, and was located on a plate containing transformants derived from Streptococcus strain GX7809 (one of the three Streptococcus strains from which DNA was isolated for cloning.) The positive colony was streaked out on an immunoassay plate (containing 100 ug/ml ampicillin, as above) to obtain a purified transformant strain. The nitrocellulose sheet was processed as above, and only a few positives were found among hundreds of negative colonies. It appeared that the original transformant was unstable, so the restreaking process was repeated, and only one positive was found among hundreds of negative colonies. Another round of restreaking produced a plate containing mostly positive colonies. One of the positive colonies, a derivative which was apparently more stable than the original positive transformant, was isolated and designated *E. coli* strain GX7820. Samples of *E. coli* GX7820 have been deposited at the American Type Culture Collection in Rockville, Maryland and given the accession number ATCC No. 53460.

In addition to the original positive colony, several small but strongly positive spots, which could not be correlated with any colony, were observed. These spots yielded no positive progeny on restreaking.

A standard procedure was used to isolate plasmid DNA from *E. coli* GX7820, and the plasmid DNA was analyzed by restriction analysis followed by gel electrophoresis. The strain was found to contain two types of plasmids. One plasmid (designated pGX1066X) appeared to be the same size as the pGX1066 cloning vector, while the other (designated pGX4530) apparently was pGX1066 containing an 11 kbp insert. Competent *E. coli* SK2267 cells then were retransformed with the mixture of plasmids isolated from GX7820, and transformants were selected on immunoassay plates containing 100 ug/ml ampicillin. Positive transformants of two types were obtained. A majority formed tiny, strongly positive colonies, most of which could not be propagated. A minority resembled GX7820 in being of more normal size and more easily propagatable. In order to clarify the cause of these results, competent *E. coli* SK2267 cells were also transformed with gel purified plasmids, as follows:

Transformation A: pGX4530 alone

Transformation B: pGX1066X alone

Transformation C: mixture of pGX4530 and pGX1066X

The results were as follows:

Transformation A: tiny, strongly positive colonies, most of which could not be propagated.

Transformation B: no transformants

Transformation C: many tiny, strongly positive non-propagatable colonies (as in trans. A) with about 20% of the positives resembling GX7820, i.e. of normal size and propagatable.

Several of the tiny, strongly positive colonies were chosen from the retransformation plates above (i.e., the transformants resulting from transformation of *E. coli* with an unfractionated plasmid preparation derived from strain GX7820 comprising a mixture of pGX1066X and pGX4530) and were restreaked to isolate propagatable strains. Plasmid DNA was isolated from two strains, and both were found to have lost the pGX1066X helper plasmid. One strain (designated *E. coli* GX7823) contained a plasmid pGX4533 in which a deletion of about 2 kbp had occurred in the 11 kbp insert found in pGX4530. Samples of *E. coli* GX7823 have been deposited at the American Type Culture Collection in Rockville, Maryland and given the accession number ATCC No. 53461. The second strain (designated *E. coli* GX7822) contained a plasmid pGX4532 which had acquired an additional 3 kbp of unidentified DNA inserted within the original 11 kbp insert, at a site very close to one end of the deletion in pGX4533.

The strains *E. coli* GX7823 (containing pGX4533) and *E. coli* GX7820 (containing pGX4530) were cultivated in L-Broth plus ampicillin. The cells were pelleted by centrifugation, lysed by incubating for 30 min at 37 °C in the presence of 0.5 mg/ml lysozyme in a buffer containing 50 mM EDTA, pH 8.0, and 2mM PMSF. Samples of the extracts were prepared for electrophoresis by heating for 5 min. at 100 °C in the buffer described by Studier [J. Mol. Biol. 79 :237-248 [1973]], and the samples were subjected to electrophoresis on a 12.5% acrylamide-SDS gel as described by Studier, *op cit.*, to separate the proteins. A standard electrophoretic (Western Blotting) technique was used to transfer the protein bands from the gel to nitrocellulose paper. The nitrocellulose was subsequently incubated (in sequence) with BSA, normal rabbit serum, peroxidase-conjugated goat anti-rabbit IgG, and 4-chloro-1-naphthol plus H₂O₂ (the same nitro-cellulose treatment as the immunochemical procedure described above). Both strains were found to produce the same IgG-binding protein bands with mobilities corresponding to molecular weights between approximately 90,000 to approximately 30,000 with a predominant band at 57,000.

Plasmid pGX4533 was subjected to restriction analysis, and a partial restriction map is shown in Figure 2. The single line represents the vector (pGX1066) sequences, while the hatched area represents the DNA that has been inserted into the plasmid vector and which contains the Protein G gene.

The 1.9 kbp Hin dIII fragment in the insert was subcloned into pGX1066, and the resulting recombinant plasmid (pGX4547) was transformed into E. coli. Western blotting of the proteins produced by this transformant (E. coli GX7841) was done as described above, and the same IgG-binding protein bands were present including the predominant 57,000 band. The transformant was also analyzed in a hemagglutination assay, as described above. Extracts of the transformant agglutinated tanned sheep erythrocytes coated with IgG3 (human myeloma protein) and with unfractionated human IgG, but uncoated erythrocytes were not agglutinated. An extract from a Protein A-producing E. coli strain agglutinated the erythrocytes coated with unfractionated IgG, but not those coated with IgG3 or uncoated erythrocytes. A control E. coli strain which produced neither Protein A nor Protein G failed to agglutinate any of the erythrocyte samples.

These results demonstrate that E. coli strains GX7841, GX7820, and GX7823 produce IgG-binding protein having the properties which are characteristics of Protein G.

EXAMPLE II

DNA and Amino Acid Sequence Data

The DNA sequence of the cloned gene was determined. This sequence is shown in Figure 3, along with the amino acid sequence specified by the DNA sequence. The data in Figure 3 are for the entire 1.9kbp Hin dIII fragment which contains the cloned Protein G gene, as described above.

It will be appreciated that because of the degeneracy of the genetic code, the nucleotide sequence of the gene can vary substantially. For example, portions or all of the gene could be chemically synthesized to yield DNA having a different nucleotide sequence than that shown in Figure 3, yet the amino acid sequence would be preserved, provided that the proper codon-amino acid assignments were observed. Having established the nucleotide sequence of the Protein G gene and the amino acid sequence of the protein, the gene of the present invention is not limited to a particular nucleotide sequence, but includes all variations thereof as permitted by the genetic code.

The Protein G protein of the present invention is not limited to a protein having the exact amino acid sequence shown in Figure 3. A protein comprising deletions or substitutions in the sequence shown in Figure 3, or additional amino acids at the amino or carboxyl terminus of the protein, are included in the present invention as long as the protein retains the desired IgG-binding properties of Protein G, described above. These variations in amino acid sequence may be achieved by chemical synthesis of the gene, or by known in vitro mutagenesis procedures, for example.

The following abbreviations are used in Figure 3:

A = deoxyadenyl
T = thymidyl
G = deoxyguanyl
C = deoxycytosyl
GLY = glycine
ALA = alanine
VAL = valine
LEU = leucine
ILE = isoleucine
SER = serine
THR = threonine
PHE = phenylalanine
CYS = cysteine
MET = methionine
ASP = aspartic acid
GLU = glutamic acid
LYS = lysine
ARG = arginine
HIS = histidine
PRO = proline
TYR = tyrosine

TRP = tryptophan
 GLN = glutamine
 ASN = asparagine

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EXAMPLE III

10 Identification of the Portions of the Protein G Molecule Responsible for the IgG-binding Activity

By examining the IgG binding activity of protein produced by *E. coli* strains carrying deleted and modified forms of the cloned protein G gene, the activity was localized to the repeating structure between
 15 amino acid residues 228 and 352 (Figure 8). The amino acid sequences of regions B1 and B2 are identical at 49 of the 55 corresponding positions in each. This repeating structure is illustrated in figure 4, where it is indicated as B1 and B2.

The 1.9 kbp *Hin* *dIII* fragment indicated in figure 2, which contains the entire coding sequence for protein G, originally isolated from *Streptococcus* GX7809, was subcloned in bacteriophage M13mp9
 20 [Messing, J., *Methods Enzymol.* 101 :20 (1983)]. The plasmid pGX4547 was digested with endonuclease *Hin* *dIII*, as was the double stranded replicative form of bacteriophage M13mp9 DNA. The latter was also treated with calf alkaline phosphatase (2 units in 15 μ l), which was present during the digestion with *Hin* *dIII*, to prevent recircularization of the vector. After extraction with phenol and precipitation with ethanol, the two digested DNA preparations were mixed and incubated with DNA ligase under ligation conditions. The
 25 ligated DNA preparation was used to transfect *E. coli* strain GX1210 (*F'* *traD36 proA+B+ lacIq/delta-lacZM15 delta-(lac-pro) supE thi zig::Tn10 hsdR2*). Transfected cells from plaques were screened for the production of protein G by colony immunoassay. One which produced a positive assay response was designated mGX4547, and was shown to have the partial restriction map illustrated in figure 5.

Double stranded replicative form DNA isolated from *E. coli* infected with mGX4547 was digested with
 30 endonuclease *Pst* I. After extraction with phenol and ethanol precipitation, the digested DNA was incubated with DNA ligase under ligation conditions in dilute solution (approximately 5 μ g digested DNA per ml). The religated DNA preparation was then used to transfect *E. coli* GX1210. Replicative form DNA was prepared from cells infected from several plaques, and the same infected cells were assayed for the production of IgG-binding protein by colony immunoassay. Several clones were found by analysis of RF DNA with
 35 restriction endonuclease *Pst* I to have lost both the 210 bp and the 415 bp *Pst* I fragments indicated in figures 5 and 6. These clones produced no active IgG-binding protein, as indicated by colony immunoassay. The truncated protein produced by these clones would be expected to contain only a portion of the structure B1, and lack all amino acid sequences distal to B1.

One of the clones obtained from the above transfection produced a positive result by colony
 40 immunoassay. Restriction analysis of RF DNA from this clone revealed that the phage DNA lacked the 415 bp *Pst* I fragment, but retained the 210 bp fragment. Furthermore, the relative intensity of the 210 bp *Pst* I fragment band on an ethidium bromide-stained agarose gel electrophoretogram suggested that the DNA carried two copies of the 210 bp fragment. DNA sequencing confirmed that the structure of this phage DNA (mGX7880) was as illustrated in figure 6. The protein encoded by the protein G gene carried on this phage
 45 DNA would be expected to contain two complete copies of the B structure, an intact B1 sequence followed by a chimera of B1 and B2. It would lack all amino acid sequences distal to B2. This structure results from the fact that the *Pst* I sites which define the 210 bp fragment are located in the B repeating structures at positions corresponding to homologous sequences, and in the same relation to the reading frame of the protein. Polyacrylamide gel electrophoretic analysis revealed that *E. coli* bearing this DNA produced a
 50 protein with IgG-binding activity of approximately the expected size [Fahnestock, et al., *J. Bacteriol.* 167 :870-880 (1986)].

These results indicate that the presence of the B repeated structure is a necessary and sufficient condition for IgG-binding activity of protein G. It was therefore concluded that the B repeating structure was the locus of IgG-binding activity in the molecule.

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EXAMPLE IV

Expression of the Protein G Gene in Bacillus Subtilis

A synthetic oligonucleotide with a sequence resembling a transcription terminator was first inserted into mGX4547. The sequence of the oligonucleotide was:

5'-pTCGAAAAAAGAGACCGGATATCCGGTCTCTTTT-3'

It is self-complementary, and when double-stranded, produces single stranded ends with the same sequence as those produced by endonuclease Sal I. To insert it into mGX4547, the phage DNA was digested with endonuclease Sal I, phenol extracted and ethanol precipitated, then incubated with the synthetic oligonucleotide (which had been denatured by heating to 70°C and slowly cooled to 23°C) and DNA ligase under ligating conditions. Ligated DNA was used to transfect *E. coli* GX1210, and clones were screened for the loss of the Sal I site and appearance of an Eco RV site, the recognition sequence for which is present on the synthetic oligonucleotide. One clone with the desired structure was designated mGX7872.

Next, sequences distal to the B2 repeated sequence were deleted from mGX7872. This was accomplished by oligonucleotide-directed *in vitro* mutagenesis. The following oligonucleotide was synthesized:

5'-pCGTTTTGAAGCGACCGGAACCTCTGTAACC-3'.

This sequence is complementary on one half to sequences in mGX4547 immediately distal to the B2 sequence, and on the other half to sequences near those coding for the C-terminus of protein G. This oligonucleotide was used as a primer for the *in vitro* synthesis of double stranded RF DNA, with mGX4547 DNA as template, using standard methods. This DNA was used to transfect *E. coli* GX1210. Plaques were screened *in situ* for the ability of phage DNA they produced to hybridize to the radioactive oligonucleotide 5'-(32P)AGCGACCGGAACCTC-3', which is complementary to the desired deleted sequence. One clone with the desired structure was identified and designated mGX7877. Its structure was verified by DNA sequence analysis. The deletion encompasses nucleotides 1651-1896 of the sequence shown in figure 3.

In order to allow fusion of the protein G coding sequence to an expression and secretion vector, a Bam HI site was created in the sequence of mGX7877 by oligonucleotide-directed *in vitro* mutagenesis. A primer oligonucleotide, with the sequence,

5'-pGGTATCTTCGATTGGATCCGGTGAATCAACAGCGAATACCG-3',

was used to promote conversion of mGX7877 single stranded DNA to duplex DNA *in vitro*. This oligonucleotide was complementary to the sequence encoding protein G in mGX7877, but includes an additional 6 nucleotides, GGATCC, which comprise the recognition sequence for endonuclease Bam HI, inserted near the beginning of the sequence encoding mature protein G (the product of removal of the secretion signal sequence). The resulting double stranded DNA was used to transfect *E. coli* GX1210. The RF DNA recovered from cells infected from plaques was screened for the presence of the Bam HI site. One with the desired structure was designated mGX8402.

A secretion vector containing the promoter and secretion signal sequence derived from a *Bacillus amyloliquefaciens* gene encoding subtilisin (apr) has been described by Vasantha and Thompson [J. Bacteriol. 165 :837-842 (1984); and U.S. Patent Application, Serial No. 618,902, filed June 8, 1984, and the continuation-in-part thereof, Serial No. 717,800, filed March 29, 1985]. This vector, pGX2134, contains a Bam HI site near the end of sequences encoding the secretion signal sequence, to which heterologous genes can be fused in order to promote their expression in *B. subtilis*, and the secretion of the protein product from the cell. In order to fuse protein G-encoding sequences to this vector, pGX2134 DNA was digested with endonucleases Bam HI and Pvu II. The RF DNA from mGX8402 was digested with endonucleases Bam HI and Sma I. After extraction with phenol and precipitation with ethanol, the digested DNA preparations were mixed and incubated with DNA ligase under ligation conditions, and the ligated DNA was used to transform *B. subtilis* GX8008 (apr deletion, npr deletion, spoOA677) protoplasts by standard methods. Transformants were selected for resistance to chloramphenicol and screened for production of protein G by colony immunoassay. A positive transformant was identified and designated GX8408 (pGX4582). The plasmid pGX4582 was shown to have the structure indicated in figure 7 by restriction analysis. It was presumably formed by insertion into pGX2134, between the Bam HI and Pvu II sites, of the Bam HI fragment of mGX8402 bearing the protein G coding sequences, plus the small Bam HI-Sma I fragment which is distal to the coding sequences in mGX8402.

Strain GX8408 was shown to produce a protein with the IgG-binding activity of protein G. This strain, where sequences distal to the B2 sequences are deleted, exhibited enhanced secretion of protein G-like material. After growth in appropriate media [Fahnestock and Fisher, J. Bacteriol. 165 :796-804 (1984)], culture supernatants and cell-associated fractions were recovered and subjected to sodium dodecyl sulfate-polyacrylamide gel electrophoretic analysis. After electrophoretic separation, protein bands were transferred

to nitrocellulose and stained immunochemically as described in Example I. Material with IgG-binding activity was found in both the culture supernatant and cell-associated fractions.

EXAMPLE V

Cloning the Gene Encoding Protein G From Streptococcus GX7805

Chromosomal DNA was isolated from a group G Streptococcus clinical isolate designated GX7805 as described in Example I. A sample of the DNA was digested with restriction endonuclease Hin dIII and subjected to electrophoresis in a 1% agarose gel under standard conditions. The usefulness of Hin dIII for this purpose was indicated by restriction analysis of pGX4533 (Example I and Figure 2) whereby it was determined that a Hin dIII site separated the protein G gene from adjacent downstream sequences which were shown to be responsible for preventing establishment of larger fragments on multicopy plasmids in E. coli. After electrophoresis, DNA fragments were transferred to nitrocellulose as described by Southern J. Mol. Biol. 98 :503 (1975). A band of approximately 2.4 kbp containing protein G-encoding sequences was located by hybridization with a radioactive probe consisting of the 1.9 kbp Hin dIII fragment indicated in Figure 2, originally isolated from Streptococcus strain GX7809. The 1.9 kbp fragment probe was purified by agarose gel electrophoresis and eluted from the gel as described in Example I, then radioactively labeled with ³²P by nick translation essentially as described by Rigby, et al. J. Mol. Biol. 113 :237 (1977). Hybridization was carried out essentially as described by Wahl et al. [Proc. Natl. Acad. Sci. USA 76 :3683-3687 (1979)]. After hybridization and washing to remove unhybridized probe, a radioactive band was located by autoradiography at a position corresponding to a length of 2.4 kbp.

A larger sample of the same GX7805 chromosomal DNA (6 ul) was digested with endonuclease Hin dIII, and the fragments were separated by electrophoresis in a 1% agarose gel (16 h at 0.35 volts/cm). After staining with ethidium bromide, portions of the gel containing bands of length 2-3 kbp (located relative to a standard consisting of endonuclease Hin dIII-digested bacteriophage lambda DNA) were excised and crushed to aid in the recovery of the DNA. The DNA was recovered after extraction with phenol as described in Example I.

Plasmid vector pGX1066 DNA (1 ug) was digested with endonuclease Hin dIII. Following extraction of the reaction mixture with phenol/chloroform/isoamyl alcohol (25:24:1), the DNA was precipitated by adding 0.1 volume 4M LiCl, 10mM EDTA, 20 ug glycogen carrier, and 2.5 vol. 95% ethanol. 0.4 ug of the digested vector DNA was incubated with the recovered Hin dIII fragments of GX7805 DNA (90% of the material recovered from 6 ug chromosomal DNA) and T4 DNA ligase (International Biotechnologies, Inc., New Haven, CT), under ligation conditions as recommended by the manufacturer, in 20 ul, for 16 h at 15 C.

E. coli SK2267 cells were transformed with 15 ul of the ligated DNA as described in Example I, and the transformed cells were plated on colony immunoassay plates and assayed for the production of immunoglobulin-binding protein as described in Example I. A positive colony was identified. Plasmid DNA isolated from this transformant was found to consist of pGX1066 with a DNA insert of 2.4 kbp. An endonuclease Hin dIII fragment comprising the insert was subcloned in a bacteriophage M13mp9 vector. The DNA sequence of the 2.4 kbp Hin dIII fragment was determined, and is presented in Figure 9.

EXAMPLE VI

Construction of Preferred Forms of the Protein G Gene for Secretion by B. subtilis

Preferred forms of Protein G are encoded by genes from which coding sequence upstream and downstream from the active B repeats (Example III) have been deleted. Such proteins, which exhibit the immunoglobulin binding activity of protein G, have enhanced stability toward proteolysis.

A. Deletion of Upstream Sequences

In order to accomplish the deletion of upstream sequences, plasmid pGX4582 (Example IV) was first modified to contain a unique cleavage site for restriction endonuclease Kpn I (see Figure 11). DNA of pGX4582 was digested with endonuclease Pvu II, which cuts at two sites, both upstream from the A repeats. After phenol extraction and ethanol precipitation, the linear plasmid fragment was then recircularized in the presence of a 5'-phosphorylated self-complementary oligonucleotide with the sequence 5'-P-CTGGGTACCCAG, which carries a recognition site for endonuclease Kpn I, by treatment with T4 DNA ligase under ligation conditions. The ligated DNA was used to transform *E. coli* SK2267, and an ampicillin resistant transformant was isolated which contained a plasmid of the desired structure, which had acquired a unique Kpn I site. This plasmid was designated pGX4590.

Next, the modified Protein G gene carried on pGX4590 was transferred to a bacteriophage M13 vector. DNA of pGX4590 was digested with endonucleases Sma I and Sal I, which excise a fragment containing the entire Protein G encoding gene. Double stranded RF DNA of bacteriophage M13mp8 was also digested with Sma I and Sal I, and both digested DNA preparations were extracted with phenol and precipitated with ethanol. The two preparations were then mixed and incubated with T4 DNA ligase under ligation conditions. The ligated DNA was used to transfect *E. coli* GX1210, and clones were screened for the presence of an insert fragment of the appropriate size. A clone containing the desired fragment was identified and designated mGX8434.

A second Kpn I site was then created in the Protein G coding sequence carried on mGX8434, using the techniques of oligonucleotide-directed mutagenesis. An oligonucleotide was synthesized with the sequence 5'-GTCAGTCTTAGGTAATGGGTACCCAGCTAAATTCATCTATCAG which is complementary to sequences carried on mGX8434 adjacent to those encoding domain B1, but carries a six-nucleotide insertion which comprises a recognition site for endonuclease Kpn I. With single stranded DNA isolated from phage mGX8434 as template and the above defined oligonucleotide as primer, double stranded RF DNA was synthesized in vitro using standard methods. This DNA was used to transfect *E. coli* GX1210, and clones were screened for the presence of a second Kpn I site. A clone with the desired structure was identified and designated mGX8441.

DNA of mGX8441 contains two Kpn I sites, both created as described above, in such a manner that deletion of the sequences between them will create an in-frame fusion of sequences upstream from the first site and those downstream from the second. This deletion was accomplished by digesting RF DNA of mGX8441 with endonuclease Kpn I, phenol-extracting and ethanol-precipitating the digested DNA, then recircularizing the larger RF fragment by incubating in dilute solution with T4 DNA ligase under ligation conditions. The ligated DNA was used to transfect *E. coli* GX1210, and clones were screened for loss of the small Kpn I fragment. A clone with the desired structure was designated mGX8442. The structure of mGX8442 at the site of deletion was verified by DNA sequencing. It encodes a protein predicted to be the same as that encoded by pGX4582 from its N-terminus through amino acid residue Ala 38 of Protein G, followed by the sequence GlyTyrPro, encoded by the Kpn I recognition sequence, then the sequence LeuProLysThrAsp (preceding domain B1) of pGX4582, and the remainder of the coding sequence of pGX4582.

In order to establish the coding sequence of mGX8442 in *B. subtilis*, the plasmid pGX4370 was used as a vector. This plasmid is similar to the plasmid pGX4312, which is described by P. Bryan et al. in U.S. Patent application 828,545 (filed February 12, 1986), except that it contains additional sequences derived from a *B. amyloliquefaciens* subtilisin-encoding gene. These sequences comprise a promoter, translation initiation sequences, and sequences encoding the secretion signal sequence, followed by a Bam HI recognition sequence. They are derived from pGX2134, which is described in Example IV. The vector also carries replication origins active in both *B. subtilis* and *E. coli*, and markers which can be selected in both organisms (kanamycin resistance in *B. subtilis* and ampicillin resistance in *E. coli*). Plasmid pGX4370 DNA was digested with endonucleases Bam HI and Hind III, phenol extracted and ethanol precipitated. Similarly, mGX8442 RF DNA was digested with endonucleases Bam HI and Hind III, phenol extracted and ethanol precipitated. The digested DNA preparations were mixed and incubated with T4 DNA ligase under ligation conditions. The ligated DNA was used to transform *E. coli* SK2267, and an ampicillin resistant transformant with the desired structure was identified by restriction analysis and designated pGX4595. Plasmid pGX4595 DNA was then used to transform protoplasts of *B. subtilis* GX8008. A kanamycin resistant transformant, designated GX8446, was shown, by analysis similar to that outlined in Example IV above, to produce protein with the immunoglobulin binding activity of Protein G, and this protein could be detected in both the extracellular medium and the cell lysate fractions.

B. Deletion of Downstream Sequences

The starting point for constructions from which downstream sequences were variously deleted was a derivative of mGX7872 (Example IV) into which a site for endonuclease Xho I was inserted by oligonucleotide-directed mutagenesis following sequences encoding domain B2 (see Figure 12). For this purpose, an oligonucleotide was synthesized with the sequence

5' -CAGTTGGTGCATCACCTCGAGGAACCTCTGTAACC

which is complementary to Protein G encoding sequences on mGX7872 immediately downstream from those encoding domain B2, but which contains a three-nucleotide insertion which creates an Xho I site. With single stranded DNA isolated from mGX7872 as template, and this oligonucleotide as primer, double stranded RF DNA was synthesized in vitro by standard methods, and used to transfect E. coli GX1210. Clones were screened for the presence of an Xho I site, and one with the desired structure was designated mGX7875. The altered sequence in mGX7875 was verified by DNA sequencing and shown to be as desired.

A Kpn I site was then inserted into mGX7875 close to sequences encoding domain B1, at the position analogous to the second Kpn I site inserted into mGX8434, which is described above. The same oligonucleotide, and methods analogous to those described above (for construction of mGX8441) were used. A clone with the desired structure was identified and designated mGX8447.

Downstream sequences derived from mGX8447 were then used to replace those present in pGX4595. For this purpose, RF DNA of mGX8447 and DNA of pGX4595 were separately digested with endonucleases Kpn I and Hind III, phenol extracted and ethanol precipitated. The digested DNA preparations were mixed and incubated with T4 DNA ligase under ligation conditions. The ligated DNA was used to transform E. coli SK2267, and an ampicillin resistant transformant carrying a plasmid with the desired structure was identified by restriction analysis, and designated pGX4596. This plasmid is similar to pGX4595, except that sequences encoding the active portion of Protein G and downstream sequences (from the Kpn I site preceding B1 to the Hind III site following the C-terminal coding sequences) are derived from mGX8447.

Plasmid pGX4596 was then used as starting point for various deletions involving downstream sequences. First, pGX4596 DNA was digested with endonuclease Xho I, which cuts at the site created by oligonucleotide-directed mutagenesis, described above, near the downstream end of sequences encoding domain B2, and Hind III, which cuts downstream from the end of the coding sequence. This digested DNA was subjected to preparative electrophoretic fractionation on a 0.7% agarose gel, and the larger of the two resulting fragments was eluted from the gel and recovered. A double stranded oligonucleotide adapter was constructed with the following structure:

5' P-TCGATCGTGCTAA
AGCACGATTTCTGA-5' P

The purified large Xho I-Hind III fragment derived from pGX4596 was recircularized in the presence of this adapter, the single stranded ends of which are complementary to the single stranded ends of the large fragment. This was accomplished by incubation of the fragment and adapter together in the presence of T4 DNA ligase under ligation conditions. The ligated DNA was used to transform E. coli SK2267, and an ampicillin resistant transformant carrying a plasmid with the desired structure was identified by screening for the presence of the endonuclease Pvu I site which is present in the adapter sequence. This plasmid was designated pGX4597. It carries a truncated Protein G gene with the following designed structure

. . . [B2]MetValThrGluValProArgSerCysEND
. . .ATGGTTACAGAGGTTCTCGATCGTGCTAAAGCTT. . .

The C-terminal Cys residue encoded by the synthetic adapter in this construction is unique in the Protein G sequence encoded by this gene. One skilled in the relevant art will recognize that such a unique residue can provide a favorable site to which chemical reactions can be directed, such as those designed to immobilize the protein on a solid matrix or to attach various chemical functionalities or other proteins to it.

A second downstream deletion encompassed sequences downstream from repeat C5. This construction made use of an endonuclease Xmn I site derived from the sequence at residue 1815 of the DNA sequence shown in Figure 8. Plasmid pGX4596 contains a total of four Xmn I sites. In order to obtain molecules cleaved only at the desired site in the Protein G coding sequence, pGX4596 DNA (5 micrograms per ml)

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20 The single stranded end of this oligonucleotide is complementary to the single stranded end of the pGX4596 fragment, generated by Hind III cleavage. The purified fragment was recircularized in the presence of this adapter by incubation with T4 DNA ligase under ligation conditions. The ligated DNA was used to transform E. coli SK2267, and an ampicillin resistant transformant containing a plasmid with the desired structure was identified by restriction analysis. This plasmid was designated pGX4599. It carries a truncated Protein G gene with the following designed structure:

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30 Plasmids pGX4597 and pGX4599 were used separately to transform protoplasts of *B. subtilis* GX8008. Kanamycin resistant transformants were selected and designated GX8455 (pGX4597) and GX8457 (pGX4599). Both strains were found to synthesize protein with the immunoglobulin binding activity of Protein G, and in both cases this protein was detected in both the extracellular medium and the cell lysate fractions.

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40 Construction of a Preferred Form of the Protein G Gene and Expression in E. coli of the Protein G
Variant Type 1

Derivatives of the Protein G gene with various deletions were fused to a regulatable promoter system
45 for advantageous expression in *E. coli*. The promoter used was a hybrid bacteriophage lambda promoter
(OL/PR) constructed by in vitro methods, and described by McKenney et al. in U.S. Patent application
534,982 (filed September 23, 1983). This promoter is carried on a plasmid pGX2606, which includes the
translation initiation site of the phage lambda cro gene, with a BamHI site, situated as follows:

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oligonucleotide was synthesized:

5' -pGTCAGTCTTAGGTAATGCAGGATCCGCTAAAATTTTCATCTATCAG-3'

BamHI

The sequence of this oligonucleotide is complementary to those in mGX7877 encoding the region between domains A2 and B1, but contains a 6-nucleotide insertion which constitutes a recognition site for endonuclease Bam HI, in the correct frame for subsequent fusion to the expression signals in pGX2606.

This oligonucleotide was used as primer to convert single-stranded mGX7877 DNA to duplex DNA in vitro. The resulting duplex DNA was used to transfect E. coli GX1210. The RF DNA recovered from cells infected from plaques was screened for the presence of the Bam HI site. One with the desired structure was designated mGX7893.

Double-stranded RF DNA of mGX7893 was digested with endonucleases Bam HI and Hind III, and the digested DNA was fractionated by agarose gel (1%) electrophoresis. The smaller of the two linear DNA bands produced, which contains sequences encoding the B1 and B2 domains of protein G, was recovered by elution from the gel. DNA of plasmid pGX2606 was digested with endonucleases Bam HI and Hind III, and the longer linear fragment recovered by phenol extraction and ethanol precipitation. The purified mGX7893 fragment was mixed with the recovered pGX2606 DNA and incubated with T4 DNA ligase under ligation conditions. Ligated DNA was used to transform E. coli GX1201, selecting for ampicillin resistance at 30°C. Transformants were screened for production of IgG binding protein at 42°C, as described in Example VII. One positive transformant was designated GX8436, and found to contain plasmid pGX4592, with the desired structure.

The N-terminal coding sequence of pGX4592, verified directly by DNA sequencing, is as follows:

fMet Asp Pro Ala Leu Pro Lys Thr Asp [B1] ...
...AGGAGGTTGT ATG GAT CCT GCA TTA CCT AAG ACT GAC ACT TAC...

The DNA sequence of the entire gene which encodes this Protein G variant is as follows:

10	20	30	40	50	60
ATGGATCCTG	CATTACCTAA	GACTGACACT	TACAAATTAA	TCCTTAATGG	TAAACATTG
AAAGGCGAAA	CACTACTGA	AGCTGTTGAT	GCTGCTACTG	CAGAAAAAGT	CTTCAACAA
TACGCTAACG	ACRACGGTGT	TGACGGTGAA	TGGACTTACG	ACGATGCGAC	TAGACCTTT
ACAGTTACTG	AAAACCCAGA	AGTGATCGAT	CGGTCTGAAT	TAACACCAGC	CGTGACAAC
TACAACTTG	TTATTAATGG	TAAACATTG	AAAGGCGAAA	CACTACTAA	AGCAGTAGAC

310	320	330	340	350	360
GCAGAAACTG	CAGAAAAAGC	CTTCAACAA	TACGCTAACG	ACAACGGTGT	TGATGGTGT
TGGACTTATG	ATGATGCGAC	TAGACCTTT	ACGGTAACTG	AAATGGTTAC	AGAGGTTCCG
GTGCTTCAA	AACGTAAABA	AGACTAA			

Under appropriate fermentation conditions, with expression induced at 42°C, continued at 39°C, strain GX8436 was shown to produce a protein of the expected size with binding activity for human IgG. This protein, which comprises the binding domains B1 and B2, has been designated protein G variant Type 1. The amino acid sequence of this variant is as follows:

5	10	15	20	25	30
1 M D P A L P K T D T Y K L I L N G K T L K G E T T T E A V D					
31 A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T F					
61 T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T L					
91 K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G V					
121 W T Y D D A T K T F T V T E M V T E V P V A S K R K E D.					

EXAMPLE VIII

Construction of Preferred Forms of the Protein G Gene for Expression in *E. coli* to Give Protein G Variants Type 2 and 3

Derivatives of the Protein G gene with various deletions were fused to a regulatable promoter system for advantageous expression in *E. coli*. The promoter used was a hybrid bacteriophage lambda promoter (OL/PR) constructed by in vitro methods, and described by McKenney et al. in U.S. Patent application 534,982 (filed September 23, 1983). This promoter is carried on a plasmid pGX2606, which includes the translation initiation site of the phage lambda cro gene, with a Ba mHI site, situated as follows:

BamHI
 ...TTGACTATTTTACCTCTGGCGGTGATAATGGTTGCATGTACTAAGGAGGTTGTATGGATCC...
-35
-10
Translation

In order to fuse modified Protein G genes derived from those carried on pGX4597 and pGX4599 at the Ba mHI site of the vector pGX2606, Ba mHI sites were created in pGX4597 and pGX4599, at the unique Kpn I sites of those plasmids. For this purpose, a self-complementary oligonucleotide linker was synthesized with the following structure:

5' P-GGATCCGTAC
CATGCCTAGG-5' P

The single stranded ends of this double stranded linker are complementary to the single stranded ends generated by digestion of the plasmids with endonuclease Kpn I, and the linker incorporates a recognition site for endonuclease Ba mHI.

DNA of plasmids pGX4597 and pGX4599 were separately digested with endonuclease Kpn I, phenol extracted and ethanol precipitated (see Figure 13). The digested DNA preparations were then incubated with the phosphorylated linker oligonucleotide and T4 DNA ligase under ligation conditions. DNA ligase was inactivated by incubation at 70°C for 3 min, and the ligated DNA preparations were then digested with endonucleases Ba mHI and Hin dIII. Each digested DNA preparation was then subjected to preparative electrophoretic fractionation on a 1% agarose gel. The fragment of mobility corresponding to a length of between 400 and 700 bp was excised, extracted from the gel, and recovered. DNA of plasmid pGX2606 was digested with endonucleases Ba mHI and Hin dIII, and subjected to preparative electrophoresis on a 0.7% agarose gel to remove the small Ba mHI-Hin dIII fragment. The larger band was excised, eluted, and recovered.

The recovered pGX2606 fragment was mixed separately with the recovered pGX4597 and pGX4599 fragments, and incubated with T4 DNA ligase under ligation conditions. The ligated DNA preparations were used separately to transform *E. coli* GX1201 (nadA::Tn10 delta 4(chlD-blu) (lambda cl857 delta Ba mHI)), a phage lambda lysogen carrying the cl857 gene encoding a thermolabile repressor protein. Transformants were selected at 30°C for ampicillin resistance and screened by a variation of the immunoassay procedure described in Example I. Cells were grown at 30°C on a cellulose acetate filter atop a nitrocellulose filter on a standard nutrient agar plate. After visible colonies had appeared, the plates were incubated at 42°C for 4-6 hours, then the nitrocellulose filter was developed as described in Example I. A positive transformant identified in this way was found to contain plasmid of the desired structure by restriction analysis. The plasmid containing pGX4597-derived sequences was designated pGX5203, and the *E. coli* strain containing this plasmid was designated GX8464. The plasmid containing pGX4599-derived sequences was designated pGX5204, and the *E. coli* strain containing this plasmid was designated GX8465.

The designed structures of the modified Protein G genes carried by pGX5203 and pGX5204 are the same at the N-terminus:

fMetAspProTyrProLeuProLysThrAsp[B1]. . .
 ...AAGGAGGTTGTATGGATCCGTACCCATTACCTAAGACTGACACTTAC. . .

5 The C-terminal sequences are the same as those of pGX4597 and pGX4599, respectively (Example VI).

Both GX8464 and GX8465 were shown to produce protein variants with the immunoglobulin binding activity of Protein G. In addition, both strains exhibited enhanced production and produced about 200 mg of recovered protein-G like material per liter of bacterial culture. Synthesis of this protein was found to be repressed at 30°C, and induced at 42°C, the mode of regulation expected of a gene under control of the hybrid phage lambda promoter OL/PR in the presence of the thermolabile repressor encoded by the cl857 gene.

The amino acid sequence of the protein G variant comprising the B1 and B2 binding domains (Type 2) produced by GX8465 is as follows:

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15      5      10      15      20      25      30
      1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
      31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
      61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
      91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
      121 V W T Y D D A T K T F T V T E M V T E V P R G D A P T E E
      151 K P E A S I P L V P L T P A T P I A K D D A K K D D T K K E
      181 D A K K P E A K K D D A K K A E T A G.
  
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The DNA sequence of the gene which encodes this Protein G variant (type 2) is as follows:

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25      10      20      30      40      50      60
      ATGGATCCGT ACCCATTACC TAAGACTGAC ACTTACAAT TAATCCTTA TGSTAAACA
      TTGAAGGCG AAACAACCTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAA AGTCTTCAA
      CAATACGCTA ACGACAACGG TGTGACGGT GAATGGACTT ACGACGATGC GACTAAGACC
      TTTACAGTTA CTGAAAAACC AGAAGTGATC GATGCGTCTG AATTAACACC AGCCGTGACA
      ACTTACAAC TTGTTATTAA TGSTAAACA TTGAAGGCG AAACAACCTAC TAAAGCAGTA
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      310      320      330      340      350      360
      GACGCAGAAA CTGCAGAAA AGCCTTCAAA CAATACGCTA ACGACAACGG TGTGATGGT
      GTTTGGACTT ATGATGATGC GACTAAGACC TTTACGGTAA CTGAAATGGT TACAGAGGT
      CCTCGAGGTG ATGCACCAAC TGAACAGAA AAACCAAGAG CAAGTATCCC TCTTGTCCG
      TTAATCCTG CAACTCCAAT TGCTAAGAT GACGCTAAGA AAGACGATAC TAAGAAGAA
35      BATGCTAAA AACCAGAGC TAAGAAGAT GACGCTAAGA AAGCTGAAC TGCCGGCTAA
  
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The amino acid sequence of the protein G variant Type 3 produced by GX8464 which comprises the B1 and B2 binding domains is as follows:

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40      5      10      15      20      25      30
      1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
      31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
      61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
      91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
45      121 V W T Y D D A T K T F T V T E M V T E V P R S C.
  
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The DNA sequence of the gene which encodes this Protein G variant (type 3) is as follows:

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50      10      20      30      40      50      60
      ATGGATCCGT ACCCATTACC TAAGACTGAC ACTTACAAT TAATCCTTA TGSTAAACA
      TTGAAGGCG AAACAACCTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAA AGTCTTCAA
      CAATACGCTA ACGACAACGG TGTGACGGT GAATGGACTT ACGACGATGC GACTAAGACC
      TTTACAGTTA CTGAAAAACC AGAAGTGATC GATGCGTCTG AATTAACACC AGCCGTGACA
      ACTTACAAC TTGTTATTAA TGSTAAACA TTGAAGGCG AAACAACCTAC TAAAGCAGTA
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      310      320      330      340      350      360
      GACGCAGAAA CTGCAGAAA AGCCTTCAAA CAATACGCTA ACGACAACGG TGTGATGGT
      GTTTGGACTT ATGATGATGC GACTAAGACC TTTACGGTAA CTGAAATGGT TACAGAGGT
      CCTCGATCGT GCTAA
  
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EXAMPLE IX

5 Construction of the Protein G Gene and Expression in E. coli to Glve Protein G Variant Type 5

Plasmid pGX4599 was used to transform E. coli GM272, a strain which lacks the dam methylase. Plasmid DNA obtained from one such transformant was digested with restriction endonuclease Cla I.
 10 Because of the absence of dam -induced methylation in this DNA, digestion produced two fragments. These fragments were recovered by phenol extraction and ethanol precipitation.

A synthetic self-complementary oligonucleotide adapter was constructed with the following sequence:

15 5'-CGCCTGGATCCAGG-3'
 3'-GGACCTAGGTCCGC-5'

This double-stranded oligonucleotide has single-stranded ends complementary to those generated by endonuclease Cla I and contains a recognition sequence for endonuclease Bam HI.

20 The 5'-phosphorylated oligonucleotide adapter was mixed with the recovered pGX4599 DNA fragment. The mixture was incubated with T4 DNA ligase under ligation conditions at a DNA concentration of approximately 10 micrograms per ml. After ligation, the recircularized DNA was used to transform E. coli SK2267, selecting for ampicillin resistance. Only one of the two fragments contains a replication origin active in E. coli and the selectable ampicillin resistance marker, so only recircularized DNA containing this
 25 fragment can transform E. coli. Transformants were screened by restriction analysis of plasmid DNA, and one containing plasmid with the desired structure (pGX5241) was identified.

Plasmids pGX5241 and pGX2606 were both digested with endonucleases Hind III and Bam HI. Digested DNA was recovered following phenol extraction and ethanol precipitation. The two digested
 30 plasmids were mixed in ligation buffer at approximately 50 micrograms DNA per ml and ligated in the presence of T4 DNA ligase. Ligated DNA was used to transform E. coli GX1201, selecting for ampicillin resistance at 30°C, and transformants were screened by restriction analysis of plasmid DNA. One containing plasmid with the desired structure (pGX5245) was designated strain GX8822. The correct structure was verified by DNA sequencing. The DNA sequence of the gene which encodes this Protein G variant is as follows:

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EXAMPLE X

Construction of Protein G Genes Encoding Protein G Variants Types 6 and 11

Plasmid pGX5204 DNA was digested with restriction endonuclease Pst I, and the long linear fragment was isolated following electrophoretic fractionation on a 1% agarose gel, and elution of the purified fragment from the gel. DNA of plasmid pGX4584 (which consists of the vector pGX1066 plus a DNA insert of 2.4 kbp containing the protein G gene isolated from Streptococcus GX7805 (see Example V), was subjected to partial digestion with Pst I, under conditions such that significant quantities of a 420 bp fragment derived from the region encoding the IgG-binding domains of protein G were present. This 420 bp Pst I fragment was isolated following agarose gel (1.5%) electrophoresis and elution from the gel.

The long Pst I fragment of pGX5204 and the 420 bp Pst I partial digest fragment from pGX4583 were mixed and ligated with T4 DNA ligase. The ligated DNA was used to transform E. coli GX1201, and transformants were screened by restriction analysis of plasmid DNA. Plasmids of two types were identified. One (pGX5247) was derived from the plasmid pGX5204 by substituting the 420 bp Pst I fragment of pGX4583 for the 210 bp fragment present in pGX5204. The strain containing pGX5247 was designated GX8825 and was shown to produce an IgG-binding protein of the expected size. The predicted structure of this protein (type 6) is as follows:

```

      1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
     31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
     61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
    91 L K G E T T T E A V D A A T A E K V F K Q Y A N D N G V D G
   121 E W T Y D D A T K T F T V T E K P E V I D A S E L T P A V T
   151 T Y K L V I N G K T L K G E T T T K A V D A E T A E K A F K
   181 Q Y A N D N G V D G V W T Y D D I T K T F T V T E M V T E V
   211 P R G D A P T E P E K P E A S I P L V P L T P A T P I A K D
   241 D A K K D D T K K E D A K K P E A K K D D A K K A E T A G.

```

The DNA sequence of the gene which encodes this Protein G variant (type 6) is as follows:

```

    35 ATGGATCCGT ACCCATTACC TAAGACTGAC ACTTACAART TAATCCTTAA TGGTAAACAA
       TTGAAGGCG AAACAACACTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGTCTTCAAA
       CAATACGCTA ACGACACACGG TGTGACGGT GAATGGACTT ACGACGATGC GACTAAGACC
       TTTACAGTTA CTGAAARACC AGAAGTGATC GATGCGTCTG AATTAACACC AGCCGTGACA
       ACTTACAAC TTGTTATTAA TGGTAAACAA TTGAAGGCG AAACAACACTAC TAAGCAGTA
       310       320       330       340       350       360
    40 GACGCAGAAA CTGCAGAAAA AGTCTTCAAA CAATACGCTA ACGACACACGG TGTGACGGT
       GAATGGACTT ACGACGATGC GACTAAGACC TTTACAGTTA CTGAAARACC AGAAGTGATC
       GATGCGTCTG AATTAACACC AGCCGTGACA ACTTACAAC TTGTTATTAA TGGTAAACAA
       TTGAAGGCG AAACAACACTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGCCTTCAAA
       CAATACGCTA ACGACACACGG TGTGATGGT GTTGGACTT ATGATGATGC GACTAAGACC
       610       620       630       640       650       660
    45 TTTACGGTAA CTGAAATGGT TACAGAGGTT CCTCGAGGTG ATGCACCAAC TGAACCAAG
       AAACCAGAG CAAGTATCCC TCTTGTTCCG TTAAGTCTCT CAACTCCAAT TGCTAAGAT
       GACGCTAAGA AAGACGATAC TAAGAAAGAA GATGCTAAAA AACCAGAGC TAAGAAGAT
       GACGCTAAGA AAGCTGAAC TGCCGCTAA

```

The sequence contains the B1, B1/B2, and B3 binding domains, the amino acid sequences of which are identical to those of protein G derived from Streptococcus GX7805, plus the adjacent proline-rich region and the "C-repeats" of protein G.

The second type of plasmid (pGX5246) isolated from among the above transformants was derived from pGX5204 by recircularization of the long Pst I fragment without an insert. In this plasmid, therefore, the short 210 bp Pst I fragment of pGX5204 is deleted. The strain containing pGX5246 was designated GX8824. The predicted structure of the protein produced by GX8824 (type 11) is shown below:

1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K A F K Q Y A N D N G V D G V W T Y D D A T K T
 61 F T V T E M V T E V P R G D A P T E P E K P E A S I P L V P
 91 L T P A T P I A K D D A K K D D T K K E D A K K P E A K K D
 121 D A K K A E T A G.

The DNA sequence of the gene (type 11) which encodes this Protein G variant is as follows:

10
 10 20 30 40 50 60
 ATGGATCCGT ACCCATTACC TAAGACTGAC ACTTACAAAT TAATCCTTAA TGGTAAACAA
 TTGAAGGCG AAACAACCTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGCCTTCAAA
 CAATACGCTA ACGACAACGG TGTGATGGT GTTTGGACTT ATGATGATGC GACTAAGACC
 TTTACGGTAA CTGAARTGGT TACAGAGGTT CCTCGAGGTG ATGCACCAAC TGAACCAGAA
 AAACCAGAAG CAAGTATCCC TCTTGTTCCTG TTAACCTCTG CAACCTCAAT TGCTAAGAGT
 15
 310 320 330 340 350 360
 GACGCTAAGA AAGACGATAC TAAGAAAGAA GATGCTAAAA AACCAGAAGC TAAGAAAGAT
 GACGCTAAGA AAGCTGAAAC TGCCGGCTAA

20 This sequence contains a single "B repeat" sequence which is a chimera of sequences derived from sequences B1 and B2 of GX7809 protein G.

EXAMPLE XI

Construction of a Protein G Gene Encoding Protein G Variant Type 7

30 Plasmid pGX4595 was used to transform *E. coli* GM272, a strain which lacks the *dam* methylase. Plasmid DNA obtained from one such transformant was digested with restriction endonuclease *Cla* I. Because of the absence of *dam* -induced methylation in this DNA, digestion produced two fragments. These fragments were recovered by phenol extraction and ethanol precipitation.

35 A synthetic self-complementary oligonucleotide adapter was constructed with the following sequence:

5'-CGCCTGGATCCAGG-3'
 3'-GGACCTAGGTCCGC-5'

40 This double-stranded oligonucleotide has single-stranded ends complementary to those generated by endonuclease *Cla* I, and contains a recognition sequence for endonuclease *Bam* HI.

45 The 5'-phosphorylated oligonucleotide adapter was mixed with the recovered pGX4595 DNA fragment. The mixture was incubated with T4 DNA ligase under ligation conditions at a DNA concentration of approximately 10 micrograms per ml. After ligation, the recircularized DNA was used to transform *E. coli* SK2267, selecting for ampicillin resistance. Only one of the two fragments contains a replication origin active in *E. coli* and the selectable ampicillin resistance marker, so only recircularized DNA containing this fragment can transform *E. coli*. Transformants were screened by restriction analysis of plasmid DNA, and one containing plasmid with the desired structure (pGX5240) was identified.

50 Plasmids pGX5240 and pGX2606 were both digested with endonucleases *Hind* III and *Bam* HI. Digested DNA was recovered following phenol extraction and ethanol precipitation. The two digested plasmids were mixed in ligation buffer at approximately 50 micrograms DNA per ml and ligated in the presence of T4 DNA ligase. Ligated DNA was used to transform *E. coli* GX1201, selecting for ampicillin resistance at 30°C, and transformants were screened by restriction analysis of plasmid DNA. One containing plasmid with the desired structure (pGX5244) was designated strain GX8821. The correct structure was verified by DNA sequencing. The DNA sequence of the gene which encodes this Protein G variant is as follows:

5

Strain GX8821 was found to produce a protein of the expected size with the ability to bind to human IgG. The predicted structure of this protein is as follows:

10

```

      5      10      15      20      25      30
1  M D P G D A S E L T P A V T T Y K L V I N G K T L K G E T T
31 T K A V D A E T A E K A P K Q Y A N D N G V D G V W T Y D D
61 A T K T F T V T E M V T E V P V A S K R K E D ,

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15

This structure contains a single IgG binding sequence B2 (from GX7809 protein G) plus several amino acid residues derived from the C-terminus of the natural protein.

20

EXAMPLE XII

25

Construction of a Protein G Gene Encoding Protein G Variant Type 8

DNA of plasmid pGX5204 was digested with endonuclease Hind III, and linear DNA was recovered by phenol extraction and ethanol precipitation. A self-complementary synthetic DNA linker was constructed with the following sequence:

30

5'-AGCTTAGCATGAAGGCCTTCATGCTA-3'
3'-ATCGTACTTCCGGAAGTACGATTCTGA-5'

35

This double-stranded oligonucleotide has single-stranded ends complementary to those generated by endonuclease Hind III, plus a recognition sequence for endonuclease Stu I. Linearized pGX5204 DNA was mixed with the 5'-phosphorylated oligonucleotide in ligation buffer and incubated with T4 DNA ligase. The ligated DNA was used to transform E. coli GX1201 and transformants were screened by restriction analysis of plasmid DNA (for the presence of the Stu I site). A transformant with the desired plasmid (pGX5254) was identified.

40

DNA of pGX5254 was digested with endonuclease Nae I. Digestion was found to be incomplete, so linear molecules were purified from the digest by agarose gel (1%) electrophoresis, eluted from the gel, and recovered. The recovered linear molecules were then digested with Stu I, and the long linear fragment recovered by phenol extraction and ethanol precipitation. Both of these enzymes leave blunt ends. The linear DNA was then recircularized by incubation at approximately 10 micrograms per ml in ligation buffer with T4 DNA ligase. The desired effect on the DNA structure is as follows:

45

50

```

...Lys Lys Ala Glu Thr Ala Gly END <-----Linker----->
...AAG AAA GCT GAA ACT GCC GGC TAA GCTTAGCATGAAGGCCTTCATGCTAAGCTT...
      -----
      NaeI   HindIII   StuI   HindIII

```



55

```

...Lys Lys Ala Glu Thr Ala Pro Ser Cys END
...AAG AAA GCT GAA ACT GCC CCT TCA TGC TAA GCTT...

```

An in-frame fusion is formed, the effect of which is to substitute a ProSerCys sequence at the C-terminus in place of the C-terminal Gly of the protein encoded by pGX5204.

The recircularized DNA was used to transform *E. coli* GX1201, and transformants were screened by restriction analysis of plasmid DNA (for loss of the *Nae*I site). One with the desired structure (pGX5255) was designated strain GX8833. This strain was shown to produce an IgG-binding protein of the expected size, with approximately one Cys residue per molecule. The structure of the C-terminal coding region of pGX5255 was verified directly by DNA sequencing.

The DNA sequence of the gene which encodes this Protein G variant is as follows:

```

10      10      20      30      40      50      60
1  ATGGATCCGT ACCCATTACC TAAGACTGAC ACTTACAAAT TAATCCTTAA TGGTAAACA
61 TTGAAGGCG AAACAACCTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGTCTTCAAA
121 CAATACGCTA ACGACAACGG TGTGACGGT GAATGGACTT ACGACGATGC GACTAAGACC
181 TTTACAGTTA CTGAAAAACC AGAAGTGATC GATGCGTCTG AATTAAACACC AGCCGTGACA
241 ACTTACAAAC TTGTTATTAA TGGTAAACA TTGAAGGCG AAACAACCTAC TAAAGCAGTA

15      310      320      330      340      350      360
301 GACGCAGAAA CTGCAGAAAA AGCCTTCAAA CAATACGCTA ACGACAACGG TGTGATGGT
361 GTTTGGACTT ATGATGATGC GACTAAGACC TTTACGGTAA CTGAAATGGT TACAGAGGTT
421 CCTCGAGGTG ATGCACCAAC TGAACAGAA AAACAGAAAG CAGTATCCC TCTTGTCCG
481 TTAACCTCTG CAACTCCAAT TGCTAAAGAT GACGCTAAGA AAGACGATAC TAAGAAAGAA
541 GATGCTAAAA AACCAGAAGC TAAGAAAGAT GACGCTAAGA AAGCTGAAAC TGCCCTTCA

20
601 TGCTAA

```

The predicted amino acid sequence of the Protein G variant comprising the B1 and B2 domains, expressed by this gene, is as follows:

```

30      5      10      15      20      25      30
1  M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
121 V W T Y D D A T K T F T V T E M V T E V P R G D A P T E P E
151 K P E A S I P L V P L T P A T P I A K D D A K K D D T K K E
181 D A K K P E A K K D D A K K A E T A P S C.

```

EXAMPLE XIII

Construction of a Protein G Gene Encoding Protein G Variant Type 9

DNA of plasmid pGX5204 was digested with endonuclease *Hind* III, and linear DNA was recovered by phenol extraction and ethanol precipitation. A double-stranded synthetic DNA linker was constructed with the following sequence:

```

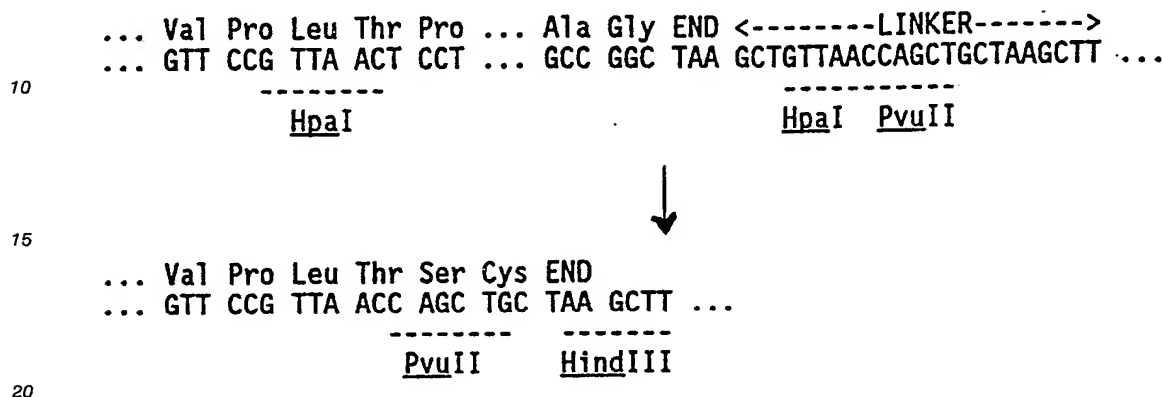
50      5'-AGCTGTTAACCAGCTGCTA-3'
      3'-CAATTGGTCGACGATTCGA-5'

```

This double-stranded oligonucleotide has single-stranded ends complementary to those generated by endonuclease *Hind* III, plus recognition sequences for endonucleases *Hpa* I and *Pvu* II. Linearized pGX5204 DNA was mixed with the 5'-phosphorylated oligonucleotide in ligation buffer and incubated with T4 DNA ligase. The ligated DNA was used to transform *E. coli* GX1201 and transformants were screened by restriction analysis of plasmid DNA (for the presence of the *Pvu* II site). The linker can be ligated to the linearized plasmid DNA in either of two orientations. Therefore, several transformants containing plasmids

which had acquired the linker (Pvu II site) were identified, some of which were expected to contain the linker in the desired orientation (e.g., pGX5267).

DNA of pGX5267 was digested with endonuclease Hpa I, and the linear DNA recovered by phenol extraction and ethanol precipitation. The linear DNA was then recircularized by incubation at approximately 10 micrograms per ml in ligation buffer with T4 DNA ligase. The desired effect on the DNA structure is as follows:



An in-frame fusion is formed, the effect of which is to detect the C-repeats present in the GX5204-encoded protein, and to substitute a SerCys sequence at the C-terminus. This creates a Cys residue which is unique in the protein. Note that if the linker were present in the opposite orientation, deletion between the two Hpa I sites would remove the Pvu II site and the Hind III site.

The recircularized DNA was used to transform E. coli GX1201, and transformants were screened by restriction analysis of plasmid DNA (for shortening of the Bam HI-Hind III fragment which contains the protein G coding sequence). Several such deleted plasmids were identified. In order to determine which had originally acquired the DNA linker in the desired orientation, the plasmids were screened for the presence of the Hind III and Pvu II sites. One with the desired structure (pGX5268) was designated strain GX8846. The DNA sequence of the gene which encodes this Protein G variant is as follows:

```

35      10      20      30      40      50      60
    1 ATGGATCCGT ACCATTACC TAAGACTGAC ACTTACAAAT TAATCCTTAA TGGTAAACA
    61 TTGAAGGCG AAACAACCTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGTCTTCAAA
    121 CAATACGCTA ACGACAACGG TGTGACGGT GAATGGACTT ACGACGATGC GACTAAGACC
    181 TTTACAGTTA CTGAAAAACC AGAAGTGATC GATGCGTCTG AATTAACACC AGCCGTGACA
    241 ACTTACAAAC TTGTTATTAA TGSTAAACA TTGAAGGCG AAACAACCTAC TAAAGCAGTA

    310      320      330      340      350      360
    301 GACGCAGAAA CTGCAGAAAA AGCCTTCAAA CAATACGCTA ACGACAACGG TGTGATGGT
    361 GTTTGGACTT ATGATGATGC GACTAAGACC TTTACGCTAA CTGAAATGGT TACAGAGGTT
    421 CCTCGAGGTG ATGCACCAAC TGAACCAGAA AAACCAGAAG CAAGTATCCC TCTTGTCCG
    481 TTAACCAGCT GCTAA

```

The predicted amino acid sequence of the Protein G variant expressed by this strain, comprising the B1 and B2 binding domains, is as follows:

```

50      5      10      15      20      25      30
    1 MDPYPLPKTD TYKL I L N G K T L K G E T T T E A V
    31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
    61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
    91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
    121 V W T Y D D A T K T F T V T E M V T E V P R G D A P T E P E
    151 K P E A S I P L V P L T S C .

```

EXAMPLE XIV

Construction of a Protein G Gene Encoding Protein G Variant Type 10

5

Plasmid pGX4599 was used to transform E. coli GM272, a strain which lacks the dam methylase. Plasmid DNA obtained from one such transformant was partially digested with restriction endonuclease Cla I under conditions where significant quantities of full-length linear DNA were formed. There are two Cla I sites in pGX4599. Because of the absence of dam -induced methylation in this DNA, both of these sites are available for cleavage by Cla I. The once-cut linear DNA is therefore of two types. This linear DNA was purified by agarose gel electrophoretic fractionation and elution from the gel, followed by digestion with endonuclease Xho I. The longest fragment so generated was again purified by agarose gel electrophoresis, eluted and was then recovered.

15 A double-stranded synthetic oligonucleotide adapter was constructed with the following sequence:

5'-CGACGTCCC-3'
3'-TGCAGGGAGCT-5'

20

This oligonucleotide has single-stranded ends complementary to those generated by endonucleases Cla I and Xho I, respectively, and a recognition site for endonuclease Aat II.

25 The purified Cla I-Xho I fragment from pGX4599 was mixed with the 5'-phosphorylated adapter oligonucleotide in ligation buffer and incubated with T4 DNA ligase. The ligated DNA was used to transform *E. coli* DH5alpha (F-, endA1, hsdR17, supE44, thi-1, recA1, gyrA96, relA1, delta (argF-lacZYA)U169, phi80dlacZdeltaM15; available from Bethesda Research Laboratories, Inc.), and transformants were screened by restriction analysis of plasmid DNA (for decrease in the size of the Bam HI-Hind III fragment containing the protein G coding sequences). One containing a plasmid with the desired structure (pGX5265) was identified.

30 Joining the Cla I and Xho I ends of the linear molecule through the synthetic adapter oligonucleotide produces an in-frame fusion:

35 ... Glu Val Ile Asp Ala ... Val Pro Arg Gly Asp ...
 ... GAA GTG ATC GAT GCG ... GTT CCT CGA GGT GAT ...

 ClaI XhoI

40

↓

... Glu Val Ile Asp Val Pro Arg Gly Asp ...
... GAA GTG ATC GAC GTC CCT CGA GGT GAT ...

AatII

45

45

In order to fuse the modified Protein G gene carried on pGX5265 at the Bam HI site of the vector pGX2606, a Bam HI site was created in pGX5265 at the unique Kpn I sites of that plasmid. For this purpose, a self-complementary oligonucleotide linker was synthesized with the following structure:

50

5' P-GGATCCGTAC
CATGCCTAGG-5' P

55

The single-stranded ends of this double-stranded linker are complementary to the single-stranded ends generated by digestion of the plasmid with endonuclease Kpn I, and the linker incorporates a recognition site for endonuclease Bam HI.

- DNA of plasmid pGX5265 was digested with endonuclease Kpn I, phenol extracted and ethanol precipitated. The digested DNA preparation was then incubated with the phosphorylated linker oligonucleotide and T4 DNA ligase under ligation conditions. DNA ligase was inactivated by incubation at 70 °C for 5 min, and the ligated DNA preparation was then digested with endonucleases Bam HI and Hind III. The digested DNA preparation was then subjected to preparative electrophoretic fractionation on a 1.4% agarose gel. Two DNA fragments were observed on the ethidium bromide-stained gel, and the fragment of greater mobility was excised, extracted from the gel, and recovered. DNA of plasmid pGX2606 was digested with endonucleases Bam HI and Hind III, and the large linear fragment recovered by phenol extraction and ethanol precipitation.
- The recovered pGX2606 fragment was mixed with the recovered pGX5265 fragment, and incubated with T4 DNA ligase under ligation conditions. The ligated DNA preparation was used to transform E. coli GX1201. Transformants were selected at 30 °C for ampicillin resistance and screened by restriction analysis of plasmid DNA (for the correctly sized Bam HI-Hind III fragment). One was found to contain plasmid of the desired structure, pGX5266. This strain was designated GX8844.
- The DNA sequence of the gene which encodes this Protein G variant is as follows:

```

      10      20      30      40      50      60
ATGGATCCGT ACCATTACC TAAGACTGAC ACTTACAAAT TAATCCTTAA TGGTAAACAA
20 TGGAAAGGCG AAACAACACTAC TGAAGCTGTT GATGCTGCTA CTGCAGAAAA AGTCTTCAAA
CAATACGCTA ACGACAACGG TGTGACGGT GAATGGACTT ACGACGATGC GACTAAGACC
TTTACAGTTA CTGAAAACCC AGAAGTGATC GACGTCCTTC GAGGTGATGC ACCAACTGAA
CCAGAAAAAC CAGAAGCAAG TATCCCTCTT GTTCCGTTAA CTCCTGCAAC TCCAATTGCT

      310      320      330      340      350      360
AAAGATGACG CTAAGAAAGA CGATACTAAG AAAGAAGATG CTA AAAAACC AGAAGCTAAG
25 AAAGATGACG CTAAGAAAGC TGAACTGCC GGTAA

```

The predicted amino acid sequence of the Protein G variant expressed by this strain, comprising the single domain B1, is as follows:

```

      5      10      15      20      25      30
1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
61 F T V T E K P E V I D V P R G D A P T E P E K P E A S I P L
91 V P L T P A T P I A K D D A K K D D T K K E D A K K P E A K
35 121 K D D A K K A E T A G,

```

EXAMPLE XV

Immobilization of Single Domain Protein G Variants on Tresyl-Activated Sepharose 4B

- The freeze-dried powder (Pharmacia) of Tresyl-activated Sepharose 4B was suspended in 1 mM HCl. After washing the gel on a sintered glass filter with 1 mM HCl, it was sucked dry by aspiration. Protein G variants were dissolved in 0.1 M NaHCO₃ containing 0.5 M NaCl at pH 8.0 to a concentration of 5 mg/ml. About 1 g of the damp gel was added to about 1 ml of the protein solution. The suspension was then rotated end-over-end at 4 °C or room temperature overnight. Thereafter, the gel was treated with a 0.1 M Tris buffer pH 8.0 for a few hours. The gel was then washed with the coupling buffer and three cycles of a pH 4 buffer (0.1 M sodium acetate, 0.5 M NaCl) and a pH 8 buffer (0.1 M Tris, 0.5 M NaCl). The gel was then stored in phosphate buffered saline (50 mM phosphate, 0.15 M NaCl, 0.005% NaN₃ pH 7-7.4) at 4 °C.

EXAMPLE XVI

Characterization of the Immobilized Protein G Variants

Three single domain Protein G variants--Type 5 (B2), Type 10 (B1) and Type 11 (B1/B2)--were characterized. Typically, the immobilized proteins from Example XV were packed in medium pressure glass chromatography columns and connected to an HPLC system.

The extent of immobilization was determined by the difference in absorbance at 280 nm before and after immobilization. Interfering elements in the reaction were removed by dialysis. Alternatively, any standard protein quantitation assay (e.g., BCA, Lowry or Coomassie blue) could be used to determine the extent of protein immobilization. The coupling and capacity results are summarized in Table 1. To determine IgG binding capacity, human serum was applied onto the column. After the column was washed extensively with PBS, bound IgG was eluted with 5 mM ammonium acetate (pH 5), 1.0 M acetic acid and equilibrated with PBS at the end. The amount of IgG eluted was quantitated by absorbance at 280 nm using an extinction coefficient of 1.4.

Table 1

Types	Protein G coupled/ml gel	Coupling efficiency	Human IgG bound/ml gel
5	3.57 mg	75%	16.6 mg
10	4.04 mg	78%	10.1 mg
11	3.84 mg	81%	11.12 mg

The binding characteristics of the immobilized variants toward F_c , F_{ab} , $F(ab')_2$ and IgG were then examined. After the columns were equilibrated with PBS, IgG or its proteolytic fragments or mixtures thereof were applied to the column. Extensive washing with PBS was then carried out. The column was then eluted with 5 mM ammonium acetate pH 5, 0.5 M ammonium acetate pH 3, 1.0 M acetic acid and finally equilibrated with PBS pH 7.0. The amount of protein was quantitated by measuring absorbance at 280 nm. The fractions were also analyzed by SDS-PAGE to ascertain the quality of the product.

F_c fragment (1.0 to 1.3 mg loaded) was applied to immobilized variants Types 5, 10 and 11. The immobilized Type 5 variant was in a 1.16 ml column and the Types 10 and 11 were in 0.75 ml columns. The results appear in Table 2:

Table 2

The Binding of F_c Fragments to Immobilized Variants Under Different Conditions						
	Type 5		Type 10		Type 11	
	mg ¹	% ²	mg	%	mg	%
Initial flow through	0.17	18	0.05	5	0.11	8
pH = 5	0.04	4	0.00	0	0.00	0
pH = 3	0.13	14	0.31	29	0.34	25
1.0 M Acetic acid	0.35	38	0.39	37	0.41	31
PBS equilibration	0.24	26	0.31	29	0.49	36

¹Based on A_{280} .

²Expressed as the percentage of the total material recovered.

With Types 10 and 11, 100% of the F_c fragment loaded was recovered in the various fractions. With Type 5, 93% of the F_c fragment loaded was recovered in the various fractions.

The results for IgG binding (1.0 to 4.6 mg loaded) to immobilized variants Types 5 (1.16 ml column), 10 and 11 (0.75 ml columns) appear in Table 3:

Table 3

The Binding of IgG to Immobilized Variants Under Different Conditions						
	Type 5		Type 10		Type 11	
	mg ¹	% ²	mg	%	mg	%
Initial flow through	0.00	0	0.00	0	0.49	11
pH = 5	ND ³	ND	0.00	0	ND	ND
pH = 3	0.02	2	0.00	0	1.62	35
1.0 M Acetic acid	0.40	51	0.16	100	1.87	40
PBS equilibration	0.37	47	0.00	0	0.66	14

¹Based on A₂₈₀.²Expressed as the percentage of the total material recovered.³ND = Not Done

With Type 5, 79% of the loaded IgG was recovered in the various fractions. With Type 10, 16% of the loaded IgG was recovered in the various fractions. With Type 11, 100% of the loaded IgG was recovered in the various fractions.

The results for Fab binding (1.0 to 1.1 mg loaded) to immobilized variants Type 5 (1.16 ml column), Type 10 and Type 11 (0.75 ml columns) appear in Table 4:

Table 4

The Binding of Fab Fragments to Immobilized Variants Under Different Conditions						
	Type 5		Type 10		Type 11	
	mg ¹	% ²	mg	%	mg	%
Initial flow through	0.57	83	0.29	66	0.59	48
pH = 5	0.00	0	0.00	0	0.07	14
pH = 3	0.00	0	0.00	0	0.00	0
1.0 M Acetic acid	0.00	0	0.00	0	0.00	0
PBS equilibration	0.12	17	0.15	34	0.33	38

¹Based on A₂₈₀.²Expressed as the percentage of the total material recovered.

With Type 5, 69% of the loaded Fab was recovered in the various fractions. With Type 10, 44% of the loaded Fab was recovered in the various fractions. With Type 11, 87% of the loaded Fab was recovered in the various fractions.

The results for F(ab')₂ binding (1.0 mg loaded) to immobilized variants Type 5 (1.16 ml column), Type 10 and Type 11 (0.75 ml columns) appear in Table 5:

Table 5

The Binding of F(ab') ₂ to Immobilized Variants Under Different Conditions						
	Type 5		Type 10		Type 11	
	mg ¹	% ²	mg	%	mg	%
Initial flow through	0.32	75	0.18	55	0.42	60
pH = 5	0.04	9	0.00	0	0.12	6
pH = 3	0.00	0	0.00	0	0.00	0
1.0 M Acetic acid	0.00	0	0.00	0	0.00	0
PBS equilibration	0.07	16	0.14	45	0.33	34

¹Based on A₂₈₀.²Expressed as the percentage of the total material recovered.

With Type 5, 43% of the loaded F(ab')₂ was recovered in the various fractions. With Type 10, 31% of the loaded F(ab')₂ was recovered in the various fractions. With Type 11, 86% of the loaded F(ab')₂ was recovered in the various fractions.

As shown in Table 2, the binding of F_c to these three immobilized variants is quite similar. However, there are notable differences in the way IgG interacts with these variants. Type 10 (B1) binds IgG very tightly and irreversibly under the elution conditions. Type 5 (B2) also binds IgG quite tightly but reversibly. With Type 11, the binding is moderate and shows the potential to fractionate IgG's into subclasses, since IgG's elute in different fractions.

In all cases, the immobilized variants exhibited much weaker binding to Fab and F(ab')₂ fragments in comparison to IgG and Fc fragments. Therefore, these immobilized variants are useful for separating IgG and Fc fragments from Fab and F(ab')₂ fragments.

Since both immobilized Type 10 and Type 11 variants show some affinity for F_{ab} fragments, the immobilized Type 5 variant stands out as a candidate for isolating F_{ab}'s. To illustrate the potential to purify F_{ab}'s, a mixture of F_c, F(ab')₂, IgG and fluorescein labeled F_{ab} was applied to a Type 5 column. Almost all the fluorescence was recovered in the flow through. To verify that the lack of binding was not due to fluorescein modification, in a separate experiment, a mixture containing fluorescein-labeled Fc fragment was chromatographed on the column. In this case, the majority of the fluorescence bound to the column which showed that the fluorescein modification did not affect the binding characteristics of the column.

EXAMPLE XVII

Immobilization of a Cysteine Containing Variant on a Maleimide-Activated Sepharose Derivative

AH-Sepharose (Pharmacia) was swollen in water and washed with 0.5 M sodium chloride, water and 0.1 M sodium phosphate pH 7.0. To the gel suspension, sulfosuccinimidyl 4-(p-maleimidophenyl) butyrate (Pierce) was added and stirred at room temperature for one hour. The gel was then washed with 0.1 M sodium phosphate pH 7.0 buffer. About 6 mg of the cysteine containing variant Type 3 was dissolved in the pH 7.0 buffer (1.1 ml). The suction-dried activated gel was then added to the protein solution. This suspension was rotated end-to-end at room temperature overnight. At this point, excess reactive groups were blocked by adding Tris and β-mercaptoethanol to the suspension and rotated for three hours at room temperature. After the incubation, the gel was washed with the coupling buffer and three cycles of a pH 4 buffer (0.1 M acetate, 0.5 M sodium chloride) and a pH 8 buffer (0.1 M Tris, 0.5 M sodium chloride). The gel was stored in phosphate buffered saline at 4°C.

The extent of immobilization was determined by the difference in absorbance at 280 nm before and after immobilization. Interfering elements in the reaction were removed by dialysis. Alternatively, any standard protein quantitation assay (e.g., BCA, Lowry or Coomassie blue) could be used to determine the

extent of protein immobilization.

EXAMPLE XVIII

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Determination of the Binding Capacity of Maleimide Immobilized Protein G Variants

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After the immobilized protein was packed into a column (0.7 x 2.6 cm), it was washed with 1.0 M acetic acid and reequilibrated with PBS (pH 7.0). Either purified monoclonal antibodies, serum or other crude starting material was then applied onto the column. After the column was washed extensively with PBS, it was eluted with 5 mM ammonium acetate (pH 5), 1.0 M acetic acid and equilibrated with PBS at the end.

15 The amount of protein was quantitated by absorbance at 280 nm using extinction coefficients of 1.4 and 1.49 for human and mouse antibodies, respectively.

This one ml column contained 4.89 mg of Protein G variant Type 3 and bound 29.5 mg of human IgG and 20 mg of a mouse monoclonal IgG1 antibody.

20 It is believed that the introduction of a cysteine residue into the protein and the use of a thiol-specific chemistry for immobilization have resulted in a protein product which is not modified extensively. Thus, its potential for binding to antibodies is much enhanced.

For comparison, the amount of Protein G variants 2 and 3 immobilized per ml of gel using various immobilization chemistries is shown in Table 6. Also shown in Table 6 is the binding capacity of immobilized variants 2 and 3 for human IgG and mouse monoclonal IgG. As can be seen in Table 6, the type 3 variant is immobilized to a much greater extent by use of maleimide chemistry. Moreover, the type 3 variant immobilized by maleimide chemistry has unexpectedly higher binding capacity for human IgG and mouse monoclonal IgG.

Table 6

30

Type	Chemistry	Protein G Immobilized Per ml of Gel	Binding Capacity Per ml of Gel:	
			Human IgG	Mouse Mono-Clonal IgG1
2	aldehyde	3.33 mg	12.4 mg	3.3 mg
2	tresyl	2.50 mg	12.5 mg	1.8 mg
3	tresyl	2.85 mg	16.7 mg	5.2 mg
3	maleimide	4.87 mg	29.5 mg	20.0 mg

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45 Having now fully described this invention, it will be appreciated by those skilled in the art that the same can be performed with a wide range of equivalent parameters of composition, conditions, and methods of preparation without departing from the spirit or scope of the invention or any embodiment thereof.

Claims

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1. A Protein G variant.
2. A Protein G variant as claimed in claim 1 which is immobilized on a solid phase support.
3. A variant as claimed in claim 1 or 2 which comprises the B2 binding domain (Type 5) and has the amino acid sequence:

55

5
 1 M D P G D A S E L T P A V T T Y K L V I N G K T L K G E T T
 31 T K A V D A E T A E K A F K Q Y A N D N G V D G V W T Y D D
 61 A T K T F T V T E M V T E V P R G D A P T E P E K P E A S I
 91 P L V P L T P A T P I A K D D A K K D D T K K E D A K K P E
 121 A K K D D A K K A E T A G.

4. A variant as claimed in claim 1 or 2 which comprises the binding domain B2 (Type 7) and has the amino acid sequence:

10
 1 M D P G D A S E L T P A V T T Y K L V I N G K T L K G E T T
 31 T K A V D A E T A E K A F K Q Y A N D N G V D G V W T Y D D
 61 A T K T F T V T E M V T E V P V A S K R K E D,

5. A variant as claimed in claim 1 or 2 which comprises the binding domain B1 (Type 10) and has the amino acid sequence:

20
 1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
 61 F T V T E K P E V I D V P R G D A P T E P E K P E A S I P L
 91 V P L T P A T P I A K D D A K K D D T K K E D A K K P E A K
 121 K D D A K K A E T A G.

6. A variant as claimed in claim 1 or 2 which comprises the hybrid binding domain B1'/B2 (Type 11) and has the amino acid sequence:

30
 1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K A F K Q Y A N D N G V D G V W T Y D D A T K T
 61 F T V T E M V T E V P R G D A P T E P E K P E A S I P L V P
 91 L T P A T P I A K D D A K K D D T K K E D A K K P E A K K D
 121 D A K K A E T A G.

7. A variant as claimed in any of claims 1 to 5 having a single domain.

8. A variant as claimed in any of claims 2 to 7 wherein the solid phase support is agarose.

9. A variant as claimed in any of claims 2 to 8 which is immobilized to the solid phase support by linkage through a cysteine group in the Protein G variant.

10. A variant as claimed in any of claims 2 to 9 wherein the solid phase support is maleimide-activated agarose.

11. A variant as claimed in claim 1 or 2 which comprises the binding domains B1 and B2 (Type 3) and has the amino acid sequence:

45
 1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
 61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
 91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
 121 V W T Y D D A T K T F T V T E M V T E V P R S C.

12. A variant as claimed in claim 1 or 2 which comprises the binding domains B1 and B2 (Type 8) and has the amino acid sequence:

55

5
1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
121 V W T Y D D A T K T F T V T E M V T E V P R G D A P T E P E
151 K P E A S I P L V P L T P A T P I A K D D A K K D D T K K E
181 D A K K P E A K K D D A K K A E T A P S C.

13. A variant as claimed in claim 1 or 2 which comprises the binding sites B1 and B2 (Type 9) and has the amino acid sequence:

15
1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
121 V W T Y D D A T K T F T V T E M V T E V P R G D A P T E P E
151 K P E A S I P L V P L T S C.

14. A variant as claimed in claim 1 or 2 which comprises the binding domains B1 and B2 (Type 1) and has the amino acid sequence:

25
1 M D P A L P K T D T Y K L I L N G K T L K G E T T T E A V D
31 A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T F
61 T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T L
91 K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G V
121 W T Y D D A T K T F T V T E M V T E V P V A S K R K E D.

15. A variant as claimed in claim 1 or 2 which comprises the binding domains B1 and B2 (Type 2) and has the amino acid sequence:

35
1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
121 V W T Y D D A T K T F T V T E M V T E V P R G D A P T E P E
151 K P E A S I P L V P L T P A T P I A K D D A K K D D T K K E
181 D A K K P E A K K D D A K K A E T A G.

16. A variant as claimed in claim 1 or 2 which comprises the binding domains B1 and B2 (Type 4) and has the amino acid sequence:

45
1 A G D P I E D T P I I R N G G E L T N L L G N G E T T L A L
31 R N E E S A T A G Y P L P K T D T Y K L I L N G K T L K G E
61 T T T E A V D A A T A E K V F K Q Y A N D N G V D G E W T Y
91 D D A T K T F T V T E K P E V I D A S E L T P A V T T Y K L
121 V I N G K T L K G E T T T K A V D A E T A E K A F K Q Y A N
151 D N G V D G V W T Y D D A T K T F T V T E M V T E V P R G D
181 A P T E P E K P E A S I P L V P L T P A T P I A K D D A K K
211 D D T K K E D A K K P E A K K D D A K K A E T A G.

17. A variant as claimed in claim 1 or 2 which comprises the binding domains B1, B1/B2, and B2 (Type 6) and has the amino acid sequence:

1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
 61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
 91 L K G E T T T E A V D A A T A E K V F K Q Y A N D N G V D G
 121 E W T Y D D A T K T F T V T E K P E V I D A S E L T P A V T
 151 T Y K L V I N G K T L K G E T T T K A V D A E T A E K A F K
 181 Q Y A N D N G V D G V W T Y D D A T K T F T V T E M V T E L
 211 P R G D A P T E P E K P E A S I P L V P L T P A T P I A K L
 241 D A K K D D T K K E D A K K P E A K K D D A K K A E T A G .

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18. A method of isolating Fab or F(ab')₂ fragments from IgG and Fc fragments, the method comprising:
 (a) contacting a sample comprising Fc fragments, IgG and at least one of Fab or F(ab')₂ fragments with a single domain Protein G variant immobilized on a solid phase support; and
 (b) washing the solid phase support with a buffer with a pH of from 5 to 8 to give the Fab and F(ab')₂ fragments in the eluate and give a solid phase support with Fc fragments and IgG bound thereon.
19. A method of affinity chromatography of a target molecule, the method comprising:
 (a) contacting a first sample comprising a target molecule-specific IgG with a Protein G variant immobilized to a solid phase support to give target molecule-specific IgG irreversibly immobilized to the solid phase support;
 (b) contacting a second sample comprising a target molecule with the solid support having the target molecule-specific IgG immobilized thereon;
 (c) washing the solid phase support with a buffer of pH 5 to 8 to elute unbound solute; and
 (d) eluting the target molecule with a buffer of pH 3.5 to 2.4 to give the target molecule in the eluate.
20. A method of fractionating the subclasses of IgG, the method comprising:
 (a) applying a sample comprising at least two subclasses of IgG to a column containing a Protein G variant immobilized to a solid phase support;
 (b) eluting the column with a continuous or discontinuous gradient comprising a buffer of pH 8 to 2.4; and
 (c) collecting fractions of eluate containing the IgG subclasses.
21. A method of isolating IgG, the method comprising:
 (a) contacting a sample comprising IgG with a Protein G variant comprising at least one cysteine residue immobilized on a solid phase support through the cysteine residue;
 (b) washing the solid phase support with a buffer of pH 5 to 8 to elute unbound solute; and
 (c) washing the solid phase support with a buffer of pH 3.5 to 2.4 to give IgG in the eluate.
22. A method of purifying IgG in a sample, the method comprising:
 (a) contacting a sample comprising IgG with a Protein G variant immobilized to a solid phase support;
 (b) washing the solid phase support with a buffer of pH 5 to 8 to give the impurities in the eluate and IgG bound to the solid phase support; and
 (c) washing the solid phase support with a buffer of pH 3.5 to 2.4 to give IgG in the eluate.
23. A nucleic acid sequence encoding for Protein G or a Protein G variant.
24. A nucleic acid sequence encoding for an active binding site or a portion thereof of Protein G or a Protein G variant.
25. Recombinant Protein G or a variant thereof.
26. A vector comprising a nucleic acid sequence encoding for Protein G or a variant of Protein G, or an active binding site thereof.
27. A vector as claimed in claim 26 which is lambda gt11, m13mp9, pBR322 or pGx1066.
28. A host transfected with a vector as claimed in claim 26 or 27.
29. A host as claimed in claim 28 which is E. coli or Bacillus subtilis.

50 Claims for the following Contracting State: ES

1. A process for the preparation of a Protein G variant, the process comprising coupling successive amino acids together.
2. A process as claimed in claim 1 additionally comprising immobilizing the variant on a solid phase support.
3. A process as claimed in claim 1 or 2 wherein the variant comprises the B2 binding domain (Type 5) and has the amino acid sequence:

5
 1 M D P G D A S E L T P A V T T Y K L V I N G K T L K G E T T
 31 T K A V D A E T A E K A F K Q Y A N D N G V D G V W T Y D D
 61 A T K T F T V T E M V T E V P R G D A P T E P E K P E A S I
 91 P L V P L T P A T P I A K D D A K K D D T K K E D A K K P E
 121 A K K D D A K K A E T A G.

4. A process as claimed in claim 1 or 2 wherein the variant comprises the binding domain B2 (Type 7) and has the amino acid sequence:

10
 1 M D P G D A S E L T P A V T T Y K L V I N G K T L K G E T T
 31 T K A V D A E T A E K A F K Q Y A N D N G V D G V W T Y D D
 61 A T K T F T V T E M V T E V P V A S K R K E D,

5. A process as claimed in claim 1 or 2 wherein the variant comprises the binding domain B1 (Type 10) and has the amino acid sequence:

20
 1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
 61 F T V T E K P E V I D V P R G D A P T E P E K P E A S I P L
 91 V P L T P A T P I A K D D A K K D D T K K E D A K K P E A K
 121 K D D A K K A E T A G.

6. A process as claimed in claim 1 or 2 wherein the variant comprises the hybrid binding domain B1'/B2 (Type 11) and has the amino acid sequence:

30
 1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K A F K Q Y A N D N G V D G V W T Y D D A T K T
 61 F T V T E M V T E V P R G D A P T E P E K P E A S I P L V P
 91 L T P A T P I A K D D A K K D D T K K E D A K K P E A K K D
 121 D A K K A E T A G.

7. A process as claimed in any of claims 1 to 5 wherein the variant has a single domain.

8. A process as claimed in any of claims 2 to 7 wherein the solid phase support is agarose.

9. A process as claimed in any of claims 2 to 8 wherein the Protein G is immobilized to the solid phase support by linkage through a cysteine group in the Protein G variant.

40 10. A process as claimed in any of claims 2 to 9 wherein the solid phase support is maleimide-activated agarose.

11. A process as claimed in claim 1 or 2 wherein the variant comprises the binding domains B1 and B2 (Type 3) and has the amino acid sequence:

45
 1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
 61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
 91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
 50 121 V W T Y D D A T K T, F T V T E M V T E V P R S C.

12. A process as claimed in claim 1 or 2 wherein the variant comprises the binding domains B1 and B2 (Type 8) and has the amino acid sequence:

55

1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
 61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
 91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
 121 V W T Y D D A T K T F T V T E M V T E V P R G D A P T E P E
 151 K P E A S I P L V P L T P A T P I A K D D A K K D D T K K E
 181 D A K K P E A K K D D A K K A E T A P S C.

13. A process as claimed in claim 1 or 2 wherein the variant comprises the binding sites B1 and B2 (Type 9) and has the amino acid sequence:

1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
 61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
 91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
 121 V W T Y D D A T K T F T V T E M V T E V P R G D A P T E P E
 151 K P E A S I P L V P L T S C.

14. A process as claimed in claim 1 or 2 wherein the variant comprises the binding domains B1 and B2 (Type 1) and has the amino acid sequence:

1 M D P A L P K T D T Y K L I L N G K T L K G E T T T E A V D
 31 A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T F
 61 T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T L
 91 K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G V
 121 W T Y D D A T K T F T V T E M V T E V P V A S K R K E D.

15. A process as claimed in claim 1 or 2 wherein the variant comprises the binding domains B1 and B2 (Type 2) and has the amino acid sequence:

1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K V F K Q Y A N D N G V D G E W T Y D D A T K T
 61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
 91 L K G E T T T K A V D A E T A E K A F K Q Y A N D N G V D G
 121 V W T Y D D A T K T F T V T E M V T E V P R G D A P T E P E
 151 K P E A S I P L V P L T P A T P I A K D D A K K D D T K K E
 181 D A K K P E A K K D D A K K A E T A G.

16. A process as claimed in claim 1 or 2 wherein the variant comprises the binding domains B1 and B2 (Type 4) and has the amino acid sequence:

1 A G D P I E D T P I I R N G G E L T N L L G N G E T T L A L
 31 R N E E S A T A G Y P L P K T D T Y K L I L N G K T L K G E
 61 T T T E A V D A A T A E K V F K Q Y A N D N G V D G E W T Y
 91 D D A T K T F T V T E K P E V I D A S E L T P A V T T Y K L
 121 V I N G K T L K G E T T T K A V D A E T A E K A F K Q Y A N
 151 D N G V D G V W T Y D D A T K T F T V T E M V T E V P R S D
 181 A P T E P E K P E A S I P L V P L T P A T P I A K D D A K K
 211 D D T K K E D A K K P E A K K D D A K K A E T A G.

17. A process as claimed in claim 1 or 2 wherein the variant comprises the binding domains B1, B1/B2, and B2 (Type 6) and has the amino acid sequence:

5
 10
 15
 20
 25
 30
 1 M D P Y P L P K T D T Y K L I L N G K T L K G E T T T E A V
 31 D A A T A E K V F K Q Y A N D N G V D G E H T Y D D A T K T
 61 F T V T E K P E V I D A S E L T P A V T T Y K L V I N G K T
 91 L K G E T T T E A V D A A T A E K V F K D Y A N D N G V D G
 121 E W T Y D D A T K T F T V T E K P E V I D A S E L T P A V T
 151 T Y K L V I N G K T L K G E T T T T K A V D A E T A E K A F K
 181 Q Y A N D N G V D G V W T Y D D A T K T F T V T E M V T E L
 211 P R G D A P T E P E K P E A S I P L V P L T P A T P I A K L
 241 D A K K D D T K K E D A K K P E A K K D D A K K A E T A G.

18. A method of isolating Fab or F(ab')₂ fragments from IgG and Fc fragments, the method comprising:
- (a) contacting a sample comprising Fc fragments, IgG and at least one of Fab or F(ab')₂ fragments with a single domain Protein G variant immobilized on a solid phase support; and
 - (b) washing the solid phase support with a buffer with a pH of from 5 to 8 to give the Fab and F(ab')₂ fragments in the eluate and give a solid phase support with Fc fragments and IgG bound thereon.
19. A method of affinity chromatography of a target molecule, the method comprising:
- (a) contacting a first sample comprising a target molecule-specific IgG with a Protein G variant immobilized to a solid phase support to give target molecule-specific IgG irreversibly immobilized to the solid phase support;
 - (b) contacting a second sample comprising a target molecule with the solid support having the target molecule-specific IgG immobilized thereon;
 - (c) washing the solid phase support with a buffer of pH 5 to 8 to elute unbound solute; and
 - (d) eluting the target molecule with a buffer of pH 3.5 to 2.4 to give the target molecule in the eluate.
20. A method of fractionating the subclasses of IgG, the method comprising:
- (a) applying a sample comprising at least two subclasses of IgG to a column containing a Protein G variant immobilized to a solid phase support;
 - (b) eluting the column with a continuous or discontinuous gradient comprising a buffer of pH 8 to 2.4; and
 - (c) collecting fractions of eluate containing the IgG subclasses.
21. A method of isolating IgG, the method comprising:
- (a) contacting a sample comprising IgG with a Protein G variant comprising at least one cysteine residue immobilized on a solid phase support through the cysteine residue;
 - (b) washing the solid phase support with a buffer of pH 5 to 8 to elute unbound solute; and
 - (c) washing the solid phase support with a buffer of pH 3.5 to 2.4 to give IgG in the eluate.
22. A method of purifying IgG in a sample, the method comprising:
- (a) contacting a sample comprising IgG with a Protein G variant immobilized to a solid phase support;
 - (b) washing the solid phase support with a buffer of pH 5 to 8 to give the impurities in the eluate and IgG bound to the solid phase support; and
 - (c) washing the solid phase support with a buffer of pH 3.5 to 2.4 to give IgG in the eluate.
23. A process for the preparation of a nucleic acid sequence encoding for Protein G or a Protein G variant, the process comprising coupling successive nucleotides together.
24. A process for the preparation of a nucleic acid sequence encoding for an active binding site or a portion thereof of Protein G or a Protein G variant, the process comprising coupling successive nucleotides together.
25. A process for the preparation of recombinant Protein G or a variant thereof, the process comprising coupling successive nucleotides together.
26. A process for the preparation of a vector the process comprising incorporating a nucleic acid sequence encoding for Protein G or a variant of Protein G, or an active binding site thereof, into nucleic acid of a vector.
27. A process as claimed in claim 26 wherein the vector is lambda gt11, m13mp9, pBR322 or pGx1066.
28. A process comprising transfecting a host with a vector as claimed in claim 26 or 27.
29. A process as claimed in claim 28 wherein the host is E. coli or Bacillus subtilis.

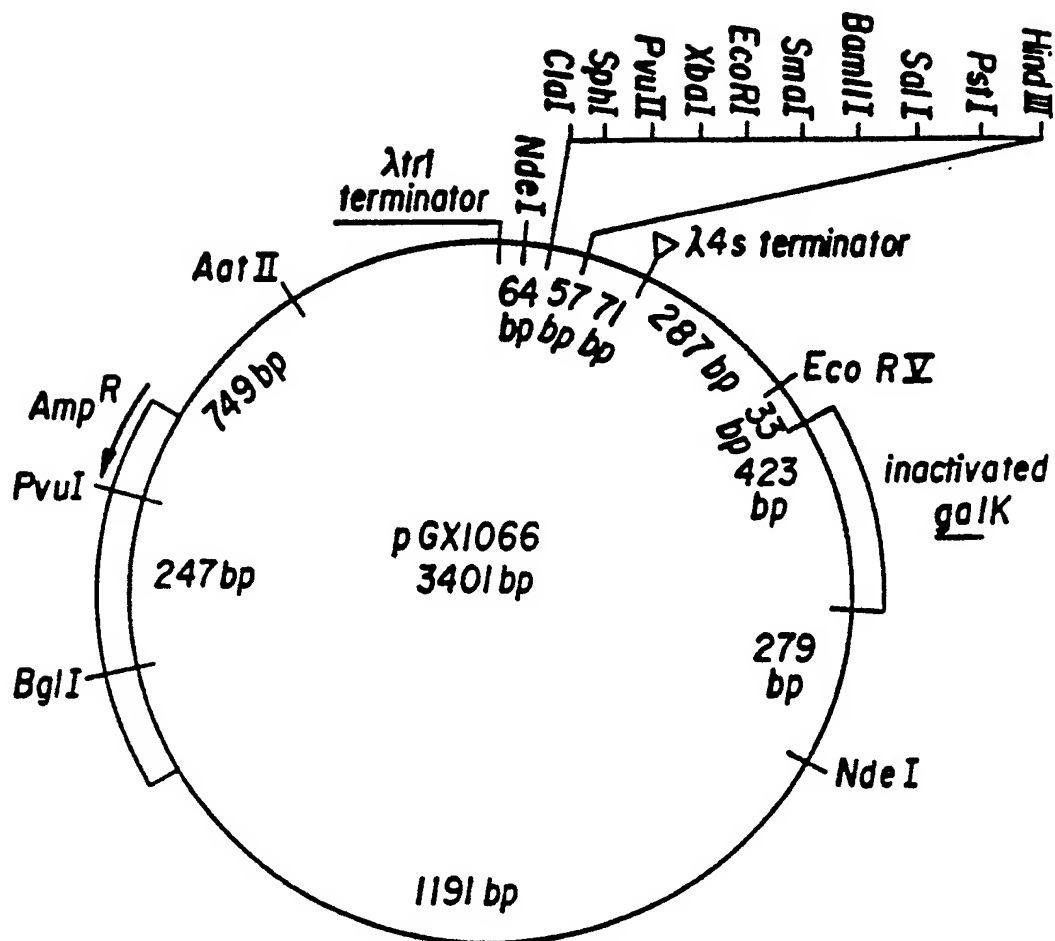
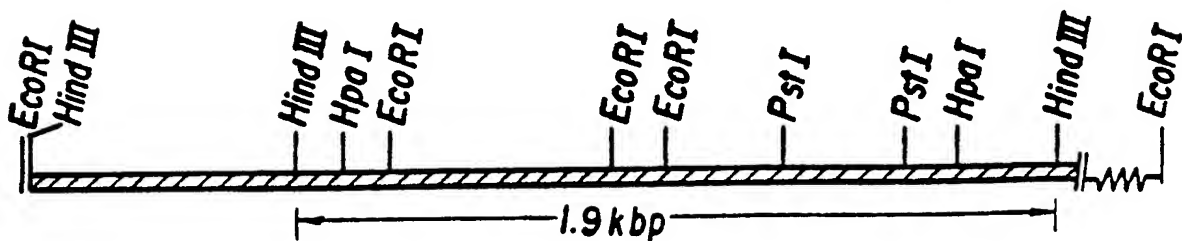


Fig. 1



PARTIAL RESTRICTION MAP OF PLASMID pGX4533

Fig. 2

AAGCTTTGGTGGAGAAATTGGCTGGCGAATCCAGCTTCACCGGTGTTTCA	50
CCAGTAGATGCTTTCTGTGGTCTTATTGACACGCACTTGTGGCGAGAGTA	100
CTAACAGTCACAGCGACGTAACTTTATTTTCCTTATGAGAGGTTAAGAA	150
AAAACGTTATTAATAGCAGAAAAGAATATTATGACTGACGTTAGGAGTT	200
TTCTCCTAACGTTTTTTTTTAGTACAAAAAGAGAATTCTCTATTATAAATA	250
AAATAAATAGTACTATAGATAGAAAATCTCATTTTTTAAAAAGTCTTGTTT	300
TCTTAAAGAAGAAAATAATTGTTGAAAAATTATAGAAAATCATTTTTTATA	350
CTAATGAAATAGACATAAGGCTAAATTGGTGAGGTGATGATAGGAGATTT	400
ATTTGTAAGGATTCCTTAATTTTATTAATTCAACAAAAATTGATAGAAAA	450
ATTAAATGGAATCCTTGATTTAATTTTATTAAGTTGTATAATAAAAAGTG	500
-35 -10	
AAATTATTAATCGTAGTTTCAAATTTGTCGGCTTTTTAATATGTGCTGG	550
CATATTAAAATTAAAAAAGGAGAAAAA	592
rbs	
LYS VAL LYS TYR 10 PHE LEU ARG LYS SER ALA PHE GLY LEU	631
AAG GTA AAA TAC TTT TTA CGT AAA TCA GCT TTT GGG TTA	
ALA 20 SER VAL SER ALA ALA PHE LEU VAL GLY SER 30 THR VAL	670
GCA TCC GTA TCA GCT GCA TTT TTA GTG GGA TCA ACG GTA	
PHE ALA VAL ASP SER PRO ILE GLU 40 ASP THR PRO ILE ILE	709
TTC GCT GTT GAT TCA CCA ATC GAA GAT ACC CCA ATT ATT	
ARG ASN GLY GLY GLU 50 LEU THR ASN LEU LEU GLY ASN SER	748
CGT AAT GGT GGT GAA TTA ACT AAT CTT CTG GGG AAT TCA	
GLU 60 THR THR LEU ALA LEU ARG ASN GLU GLU SER ALA 70 THR	787
GAG ACA ACA CTG GCT TTG CGT AAT GAA GAG AGT GCT ACA	

FIG. 3

ALA GCT	ASP GAT	LEU TTG	THR ACA	ALA GCA	ALA GCA	ALA GCG	VAL GTA	ALA GCC	80 ASP GAT	THR ACT	VAL GTG	ALA GCA	826
ALA GCA	ALA GCG	ALA GCA	ALA GCT	GLU GAA	ASN AAT	90 ALA GCT	GLY GGG	ALA GCA	ALA GCA	ALA GCT	TRP TGG	GLU GAA	865
ALA GCA	ALA GCG	ALA GCA	100 ALA GCA	ALA GCA	ASP GAT	ALA GCT	LEU CTA	ALA GCA	LYS AAA	ALA GCC	LYS AAA	ALA GCA	904
110 ASP GAT	ALA GCC	LEU CTT	LYS AAA	GLU GAA	PHE TTC	ASN AAC	LYS AAA	TYR TAT	GLY GGA	120 VAL GTA	SER AGT	ASP GAC	943
TYR TAT	TYR TAC	LYS AAG	ASN AAT	LEU CTA	ILE ATC	ASN AAC	130 ASN AAT	ALA GCC	LYS AAA	THR ACT	VAL GTT	GLU GAA	982
GLY GGC	ILE ATA	LYS AAA	ASP GAC	140 LEU CTT	GLN CAA	ALA GCA	GLN CAA	VAL GTT	VAL GTT	GLU GAA	SER TCA	ALA GCG	1021
LYS AAG	150 LYS AAA	ALA GCG	ARG CGT	ILE ATT	SER TCA	GLU GAA	ALA GCA	THR ACA	ASP GAT	GLY GGC	160 LEU TTA	SER TCT	1060
ASP GAT	PHE TTC	LEU TTG	LYS AAA	SER TCG	GLN CAA	THR ACA	PRO CCT	170 ALA GCT	GLU GAA	ASP GAT	THR ACT	VAL GTT	1099
LYS AAA	SER TCA	ILE ATT	GLU GAA	LEU TTA	180 ALA GCT	GLU GAA	ALA GCT	LYS AAA	VAL GTC	LEU TTA	ALA GCT	ASN AAC	1138
ARG AGA	GLU GAA	190 LEU CTT	ASP GAC	LYS AAA	TYR TAT	GLY GGA	VAL GTA	SER AGT	ASP GAC	TYR TAT	HIS CAC	200 LYS AAG	1177
ASN AAC	LEU CTA	ILE ATC	ASN AAC	ASN AAT	ALA GCC	LYS AAA	THR ACT	VAL GTT	210 GLU GAA	GLY GGT	VAL GTA	LYS AAA	1216
GLU GAA	LEU CTG	ILE ATA	ASP GAT	GLU GAA	ILE ATT	220 LEU TTA	ALA GCT	ALA GCA	LEU TTA	PRO CCT	LYS AAG	THR ACT	1255
ASP GAC	THR ACT	TYR TAC	230 LYS AAA	LEU TTA	ILE ATC	LEU CTT	ASN AAT	GLY GGT	LYS AAA	THR ACA	LEU TTG	LYS AAA	1294

FIG. 3A

240 GLY GGC	GLU GAA	THR ACA	THR ACT	THR ACT	GLU GAA	ALA GCT	VAL GTT	ASP GAT	ALA GCT	250 ALA GCT	THR ACT	ALA GCA	1333
GLU GAA	LYS AAA	VAL GTC	PHE TTC	LYS AAA	GLN CAA	TYR TAC	260 ALA GCT	ASN AAC	ASP GAC	ASN AAC	GLY GGT	VAL GTT	1372
ASP GAC	GLY GGT	GLU GAA	TRP TGG	270 THR ACT	TYR TAC	ASP GAC	ASP GAT	ALA GCG	THR ACT	LYS AAG	THR ACC	PHE TTT	1411
THR ACA	280 VAL GTT	THR ACT	GLU GAA	LYS AAA	PRO CCA	GLU GAA	VAL GTG	ILE ATC	ASP GAT	ALA GCG	290 SER TCT	GLU GAA	1450
LEU TTA	THR ACA	PRO CCA	ALA GCC	VAL GTG	THR ACA	THR ACT	TYR TAC	300 LYS AAA	LEU CTT	VAL GTT	ILE ATT	ASN AAT	1489
GLY GGT	LYS AAA	THR ACA	LEU TTG	LYS AAA	310 GLY GGC	GLU GAA	THR ACA	THR ACT	THR ACT	LYS AAA	ALA GCA	VAL GTA	1528
ASP GAC	ALA GCA	320 GLU GAA	THR ACT	ALA GCA	GLU GAA	LYS AAA	ALA GCC	PHE TTC	LYS AAA	GLN CAA	TYR TAC	330 ALA GCT	1567
ASN AAC	ASP GAC	ASN AAC	GLY GGT	VAL GTT	ASP GAT	GLY GGT	VAL GTT	TRP TGG	340 THR ACT	TYR TAT	ASP GAT	ASP GAT	1606
ALA GCG	THR ACT	LYS AAG	THR ACC	PHE TTT	THR ACG	350 VAL GTA	THR ACT	GLU GAA	MET ATG	VAL GTT	THR ACA	GLU GAG	1645
VAL GTT	PRO CCT	GLY GGT	360 ASP GAT	ALA GCA	PRO CCA	THR ACT	GLU GAA	PRO CCA	GLU GAA	LYS AAA	PRO CCA	GLU GAA	1684
370 ALA GCA	SER AGT	ILE ATC	PRO CCT	LEU CTT	VAL GTT	PRO CCG	LEU TTA	THR ACT	PRO CCT	380 ALA GCA	THR ACT	PRO CCA	1723
ILE ATT	ALA GCT	LYS AAA	ASP GAT	ASP GAC	ALA GCT	LYS AAG	390 LYS AAA	ASP GAC	ASP GAT	THR ACT	LYS AAG	LYS AAA	1762
GLU GAA	ASP GAT	ALA GCT	LYS AAA	400 LYS AAA	PRO CCA	GLU GAA	ALA GCT	LYS AAG	LYS AAA	ASP GAT	ASP GAC	ALA GCT	1801

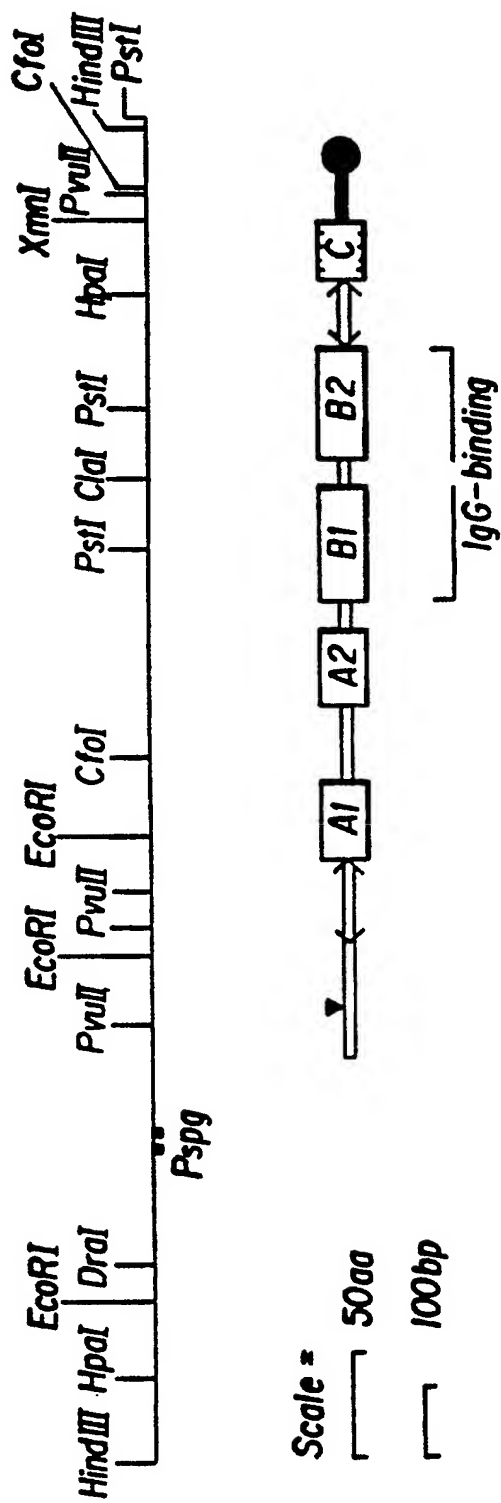
FIG. 3B

LYS AAG	410 LYS AAA	ALA GCT	GLU GAA	THR ACT	LEU CTT	PRO CCT	THR ACA	THR ACT	GLY GGT	GLU GAA	420 GLY GGA	SER AGC	1840
ASN AAC	PRO CCA	PHE TTC	PHE TTC	THR ACA	ALA GCA	ALA GCT	ALA GCG	430 LEU CTT	ALA GCA	VAL GTA	MET ATG	ALA GCT	1879
GLY GGT	ALA GCG	GLY GGT	ALA GCT	LEU TTG	440 ALA GCG	VAL GTC	ALA GCT	SER TCA	LYS AAA	ARG CGT	LYS AAA	GLU GAA	1918
ASP GAC	***												
	TAATTGTCATTATTTTTGACAAAAAGCTT 1950												

FIG. 3C

LYS AAG	410 LYS AAA	ALA GCT	GLU GAA	THR ACT	LEU CTT	PRO CCT	THR ACA	THR ACT	GLY GGT	GLU GAA	420 GLY GGA	SER AGC	1840
ASN AAC	PRO CCA	PHE TTC	PHE TTC	THR ACA	ALA GCA	ALA GCT	ALA GCG	430 LEU CTT	ALA GCA	VAL GTA	MET ATG	ALA GCT	1879
GLY GGT	ALA GCG	GLY GGT	ALA GCT	LEU TTG	440 ALA GCG	VAL GTC	ALA GCT	SER TCA	LYS AAA	ARG CGT	LYS AAA	GLU GAA	1918
ASP GAC	***												
	TAATTGTCATTATTTTTGACAAAAAGCTT 1950												

FIG. 8C



RESTRICTION MAP OF THE CLONED PROTEIN G GENE AND THE REPEATING STRUCTURE
OF ITS PROTEIN PRODUCT

Fig. 4

Fig. 5

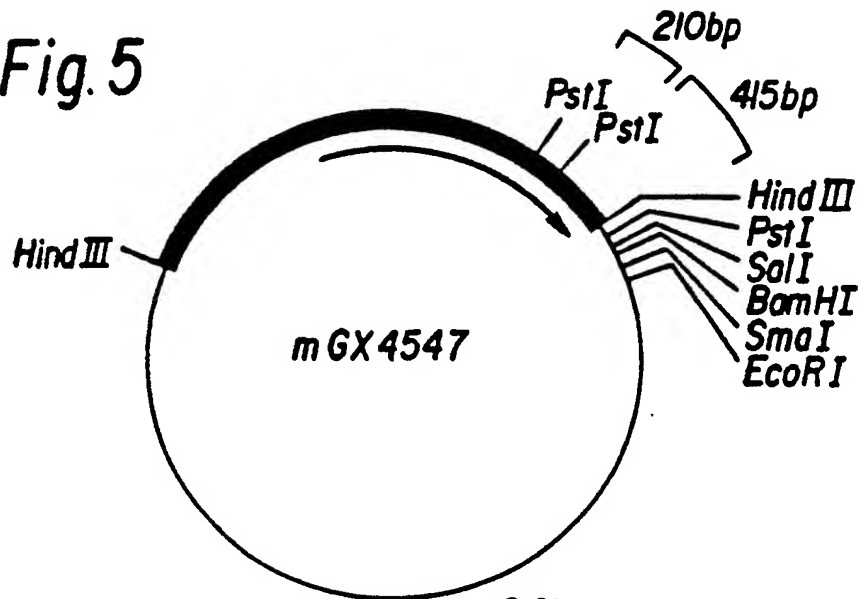


Fig. 6

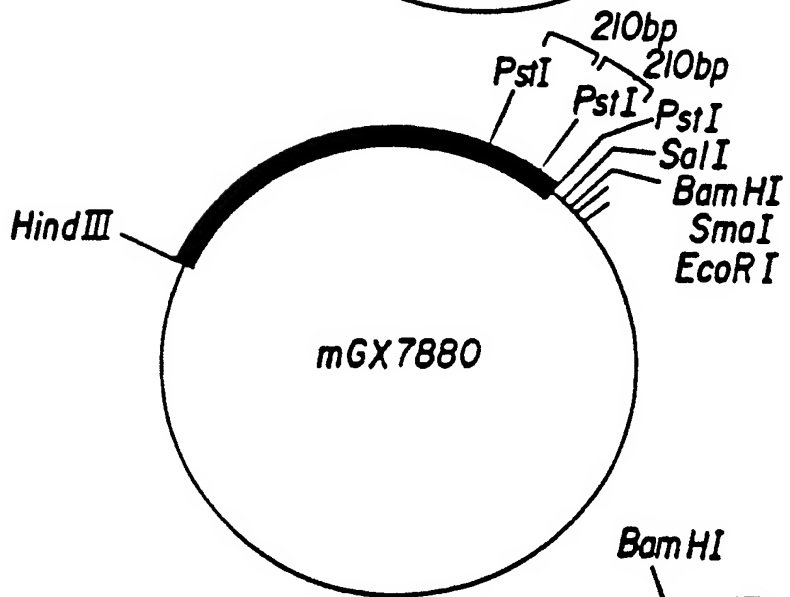
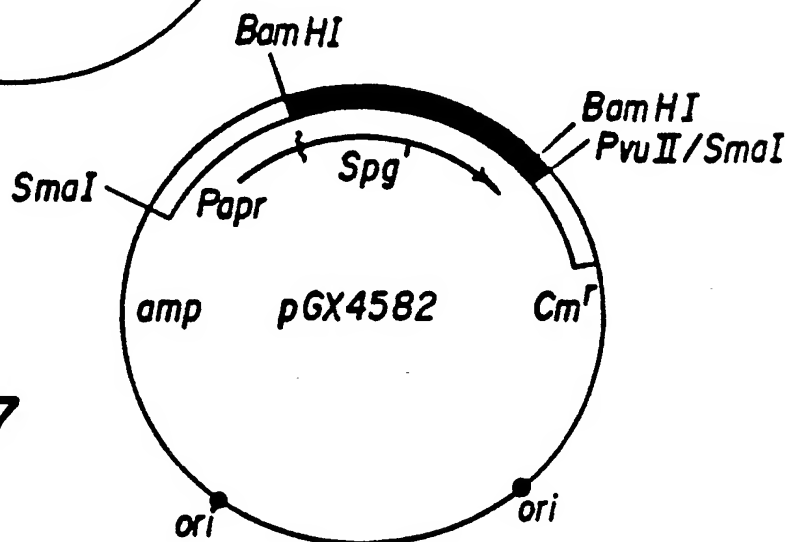


Fig. 7



AAGCTTTGGTGGAGAAATTGGCTGGCGAATCCAGCTTCACCGGTGTTTCA													50
CCAGTAGATGCTTTCTGTGGTCTTATTGACACGCACTTGTGGCGAGAGTA													100
CTAACAGTCACAGCGACGTAACTTTATTTTCCTTATGAGAGGTTAAGAA													150
AAAACGTTATTAATAGCAGAAAAGAATATTATGACTGACGTTAGGAGTT													200
TTCTCCTAACGTTTTTTTTTAGTACAAAAAGAGAATTCTCTATTATAAATA													250
AAATAAATAGTACTATAGATAGAAAATCTCATTTTTTAAAAAGTCTTGTTT													300
TCTTAAAGAAGAAAATAATTGTTGAAAAATTATAGAAAATCATTTTTTATA													350
CTAATGAAATAGACATAAGGCTAAATTGGTGAGGTGATGATAGGAGATTT													400
ATTTGTAAGGATTCCTTAATTTTATTAATTCAACAAAAATTGATAGAAAA													450
ATTAAATGGAATCCTTGATTTAATTTTATTAAGTTGTATAATAAAAAGTG													500
<div><div>-35</div><div>-10</div></div>													
AAATTATTAAATCGTAGTTTCAAATTTGTCGGCTTTTTAATATGTGCTGG													550
CATATTAAAATTAAAAAAGGAGAAAAA													592
<div><div>rbs</div></div>													
LYS AAG	VAL GTA	LYS AAA	TYR TAC	<div>10 PHE TTT</div>	LEU TTA	ARG CGT	LYS AAA	SER TCA	ALA GCT	PHE TTT	GLY GGG	LEU TTA	631
ALA GCA	<div>20 SER TCC</div>	VAL GTA	SER TCA	ALA GCT	ALA GCA	PHE TTT	LEU TTA	VAL GTG	GLY GGA	SER TCA	<div>30 THR ACG</div>	VAL GTA	670
PHE TTC	ALA GCT	VAL GTT	ASP GAT	SER TCA	PRO CCA	ILE ATC	GLU GAA	<div>40 ASP GAT</div>	THR ACC	PRO CCA	ILE ATT	ILE ATT	709
ARG CGT	ASN AAT	GLY GGT	GLY GGT	GLU GAA	<div>50 LEU TTA</div>	THR ACT	ASN AAT	LEU CTT	LEU CTG	GLY GGG	ASN AAT	SER TCA	748
GLU GAG	THR ACA	<div>60 THR ACA</div>	LEU CTG	ALA GCT	LEU TTG	ARG CGT	ASN AAT	GLU GAA	GLU GAG	SER AGT	ALA GCT	<div>70 THR ACA</div>	787

FIG. 8

ALA GCT	ASP GAT	LEU TTG	THR ACA	ALA GCA	ALA GCA	ALA GCG	VAL GTA	ALA GCC	80 ASP GAT	THR ACT	VAL GTG	ALA GCA	826
ALA GCA	ALA GCG	ALA GCA	ALA GCT	GLU GAA	ASN AAT	90 ALA GCT	GLY GGG	ALA GCA	ALA GCA	ALA GCT	TRP TGG	GLU GAA	865
ALA GCA	ALA GCG	ALA GCA	100 ALA GCA	ALA GCA	ASP GAT	ALA GCT	LEU CTA	ALA GCA	LYS AAA	ALA GCC	LYS AAA	ALA GCA	904
110 ASP GAT	ALA GCC	LEU CTT	LYS AAA	GLU GAA	PHE TTC	ASN AAC	LYS AAA	TYR TAT	GLY GGA	120 VAL GTA	SER AGT	ASP GAC	943
TYR TAT	TYR TAC	LYS AAG	ASN AAT	LEU CTA	ILE ATC	ASN AAC	130 ASN AAT	ALA GCC	LYS AAA	THR ACT	VAL GTT	GLU GAA	982
GLY GGC	ILE ATA	LYS AAA	ASP GAC	140 LEU CTT	GLN CAA	ALA GCA	GLN CAA	VAL GTT	VAL GTT	GLU GAA	SER TCA	ALA GCG	1021
LYS AAG	150 LYS AAA	ALA GCG	ARG CGT	ILE ATT	SER TCA	GLU GAA	ALA GCA	THR ACA	ASP GAT	GLY GGC	160 LEU TTA	SER TCT	1060
ASP GAT	PHE TTC	LEU TTG	LYS AAA	SER TCG	GLN CAA	THR ACA	PRO CCT	170 ALA GCT	GLU GAA	ASP GAT	THR ACT	VAL GTT	1099
LYS AAA	SER TCA	ILE ATT	GLU GAA	LEU TTA	180 ALA GCT	GLU GAA	ALA GCT	LYS AAA	VAL GTC	LEU TTA	ALA GCT	ASN AAC	1138
ARG AGA	GLU GAA	190 LEU CTT	ASP GAC	LYS AAA	TYR TAT	GLY GGA	VAL GTA	SER AGT	ASP GAC	TYR TAT	HIS CAC	200 LYS AAG	1177
ASN AAC	LEU CTA	ILE ATC	ASN AAC	ASN AAT	ALA GCC	LYS AAA	THR ACT	VAL GTT	210 GLU GAA	GLY GGT	VAL GTA	LYS AAA	1216
GLU GAA	LEU CTG	ILE ATA	ASP GAT	GLU GAA	ILE ATT	220 LEU TTA	ALA GCT	ALA GCA	LEU TTA	PRO CCT	LYS AAG	THR ACT	1255
ASP GAC	THR ACT	TYR TAC	230 LYS AAA	LEU TTA	ILE ATC	LEU CTT	ASN AAT	GLY GGT	LYS AAA	THR ACA	LEU TTG	LYS AAA	1294

B1

FIG. 8A

240 GLY GGC	GLU GAA	THR ACA	THR ACT	THR ACT	GLU GAA	ALA GCT	VAL GTT	ASP GAT	ALA GCT	250 ALA GCT	THR ACT	ALA GCA	1333
B1													
GLU GAA	LYS AAA	VAL GTC	PHE TTC	LYS AAA	GLN CAA	TYR TAC	260 ALA GCT	ASN AAC	ASP GAC	ASN AAC	GLY GGT	VAL GTT	1372
B1													
ASP GAC	GLY GGT	GLU GAA	TRP TGG	270 THR ACT	TYR TAC	ASP GAC	ASP GAT	ALA GCG	THR ACT	LYS AAG	THR ACC	PHE TTT	1411
B1													
THR ACA	280 VAL GTT	THR ACT	GLU GAA	LYS AAA	PRO CCA	GLU GAA	VAL GTG	ILE ATC	ASP GAT	ALA GCG	290 SER TCT	GLU GAA	1450
B1													
b						B2							
LEU TTA	THR ACA	PRO CCA	ALA GCC	VAL GTG	THR ACA	THR ACT	TYR TAC	300 LYS AAA	LEU CTT	VAL GTT	ILE ATT	ASN AAT	1489
b													
GLY GGT	LYS AAA	THR ACA	LEU TTG	LYS AAA	310 GLY GGC	GLU GAA	THR ACA	THR ACT	THR ACT	LYS AAA	ALA GCA	VAL GTA	1528
B2													
ASP GAC	ALA GCA	320 GLU GAA	THR ACT	ALA GCA	GLU GAA	LYS AAA	ALA GCC	PHE TTC	LYS AAA	GLN CAA	TYR TAC	330 ALA GCT	1567
B2													
ASN AAC	ASP GAC	ASN AAC	GLY GGT	VAL GTT	ASP GAT	GLY GGT	VAL GTT	TRP TGG	340 THR ACT	TYR TAT	ASP GAT	ASP GAT	1606
B2													
ALA GCG	THR ACT	LYS AAG	THR ACC	PHE TTT	THR ACG	350 VAL GTA	THR ACT	GLU GAA	MET ATG	VAL GTT	THR ACA	GLU GAG	1645
B2													
VAL GTT	PRO CCT	GLY GGT	360 ASP GAT	ALA GCA	PRO CCA	THR ACT	GLU GAA	PRO CCA	GLU GAA	LYS AAA	PRO CCA	GLU GAA	1684
370 ALA GCA	SER AGT	ILE ATC	PRO CCT	LEU CTT	VAL GTT	PRO CCG	LEU TTA	THR ACT	PRO CCT	380 ALA GCA	THR ACT	PRO CCA	1723
ILE ATT	ALA GCT	LYS AAA	ASP GAT	ASP GAC	ALA GCT	LYS AAG	390 LYS AAA	ASP GAC	ASP GAT	THR ACT	LYS AAG	LYS AAA	1762
GLU GAA	ASP GAT	ALA GCT	LYS AAA	400 LYS AAA	PRO CCA	GLU GAA	ALA GCT	LYS AAG	LYS AAA	ASP GAT	ASP GAC	ALA GCT	1801

FIG. 8B

11/22

11/22

||| a2 >
 LeuGlnAlaGlnV
 CTTCAGGCACAA
 A3 >

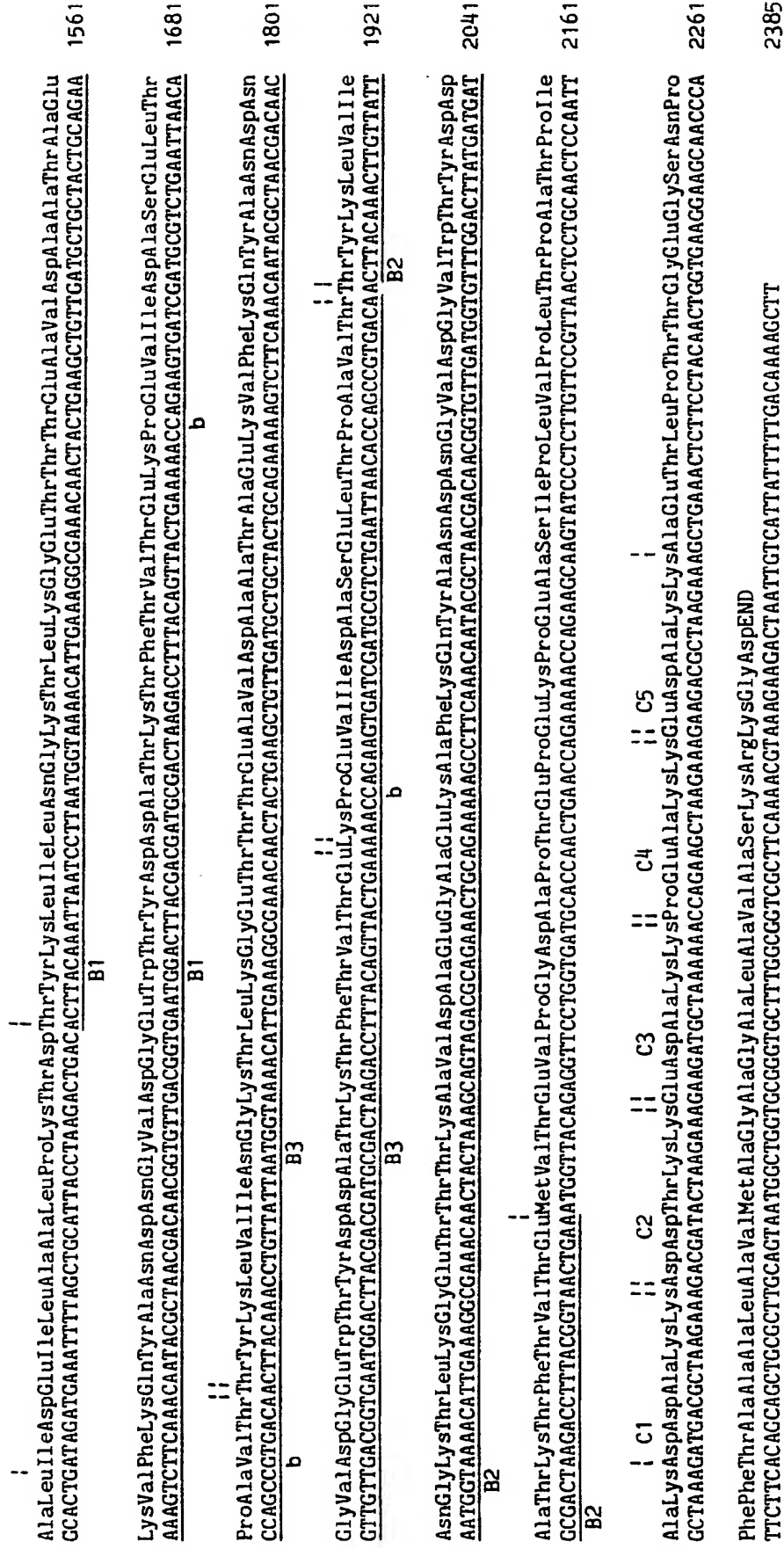
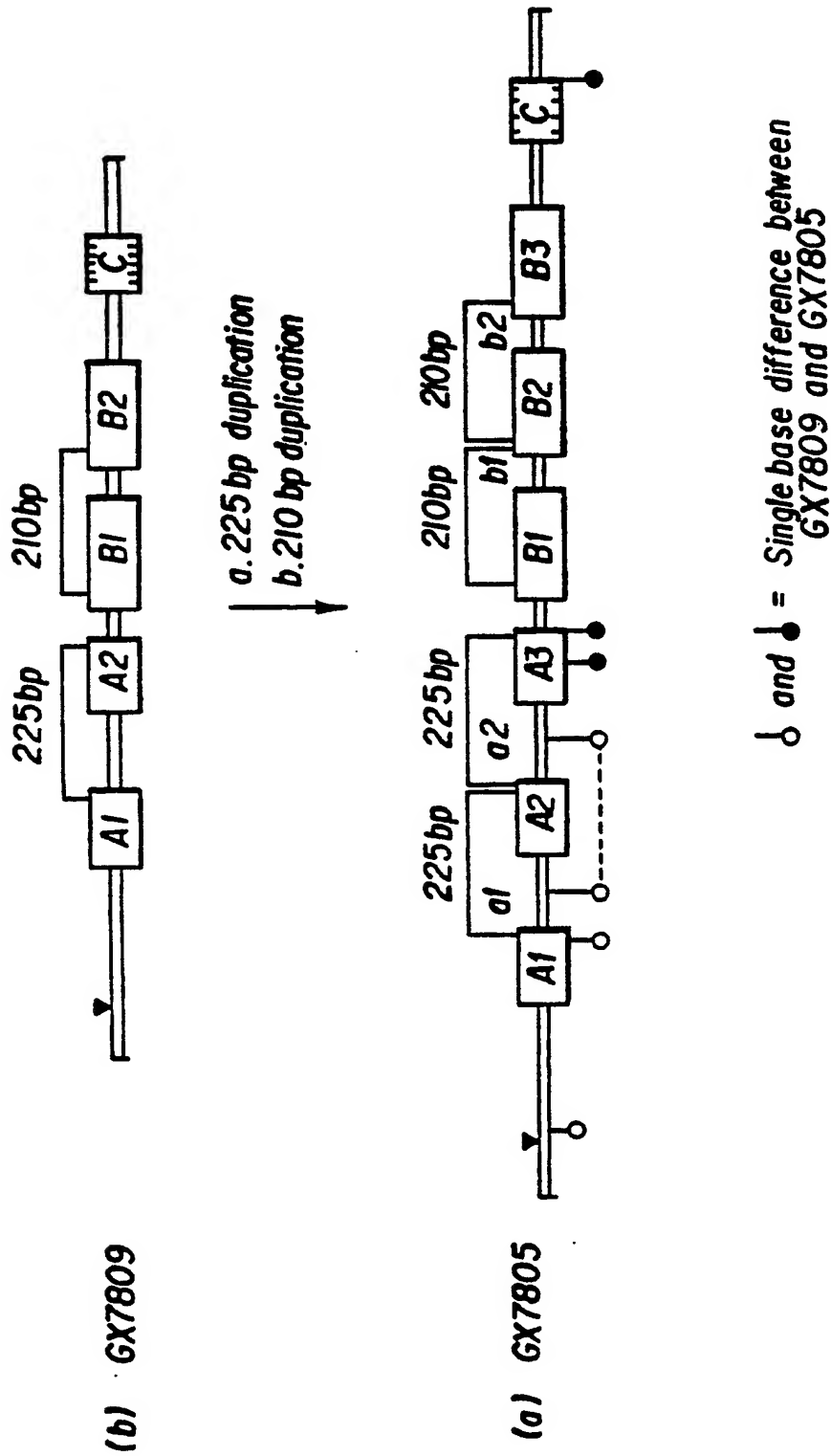


FIG. 9A



THE STRUCTURE OF PROTEIN G GENES FROM
STREPTOCOCCUS STRAINS GX7805 AND GX7809

Fig. 10

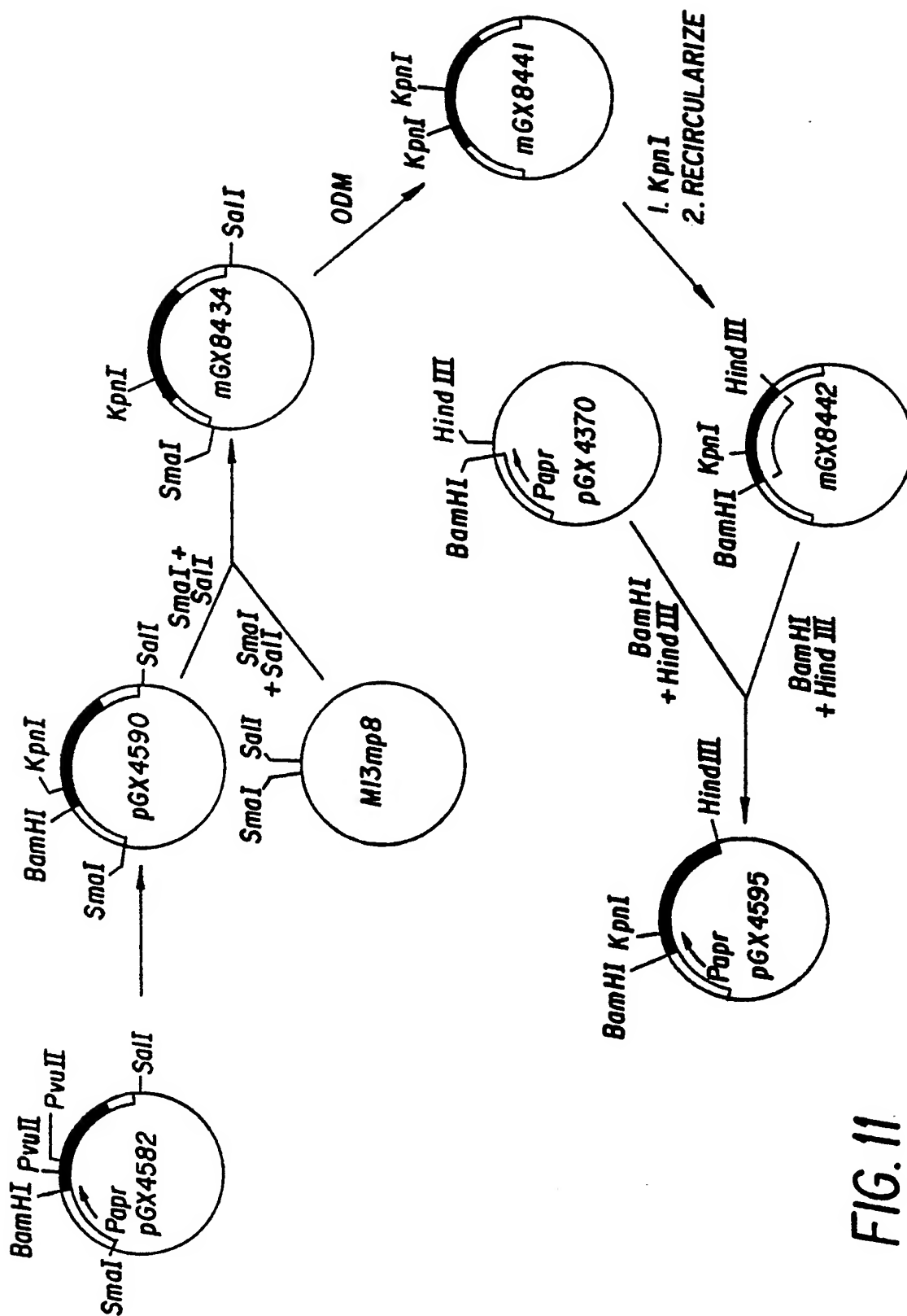


FIG. 11

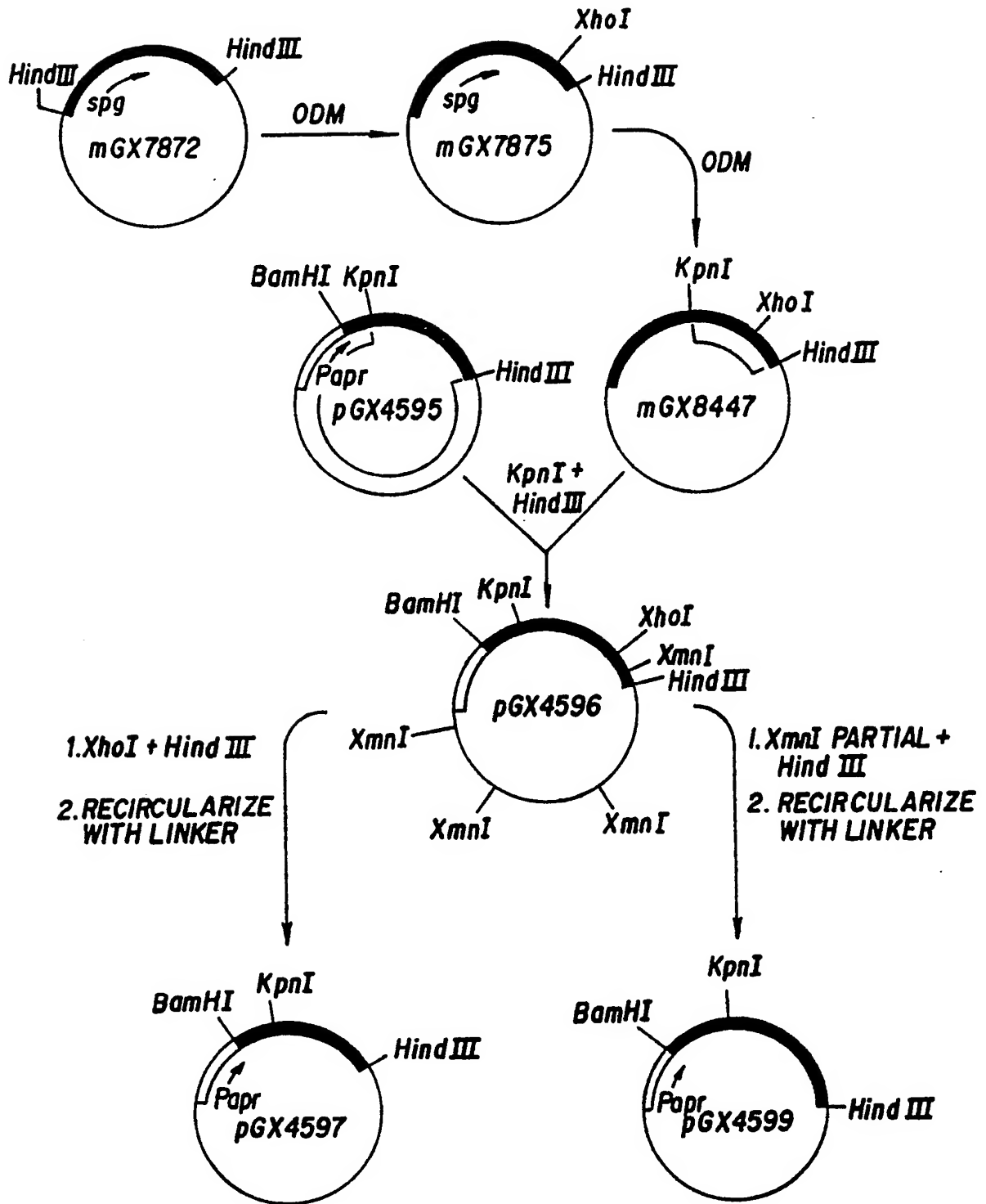


FIG.12

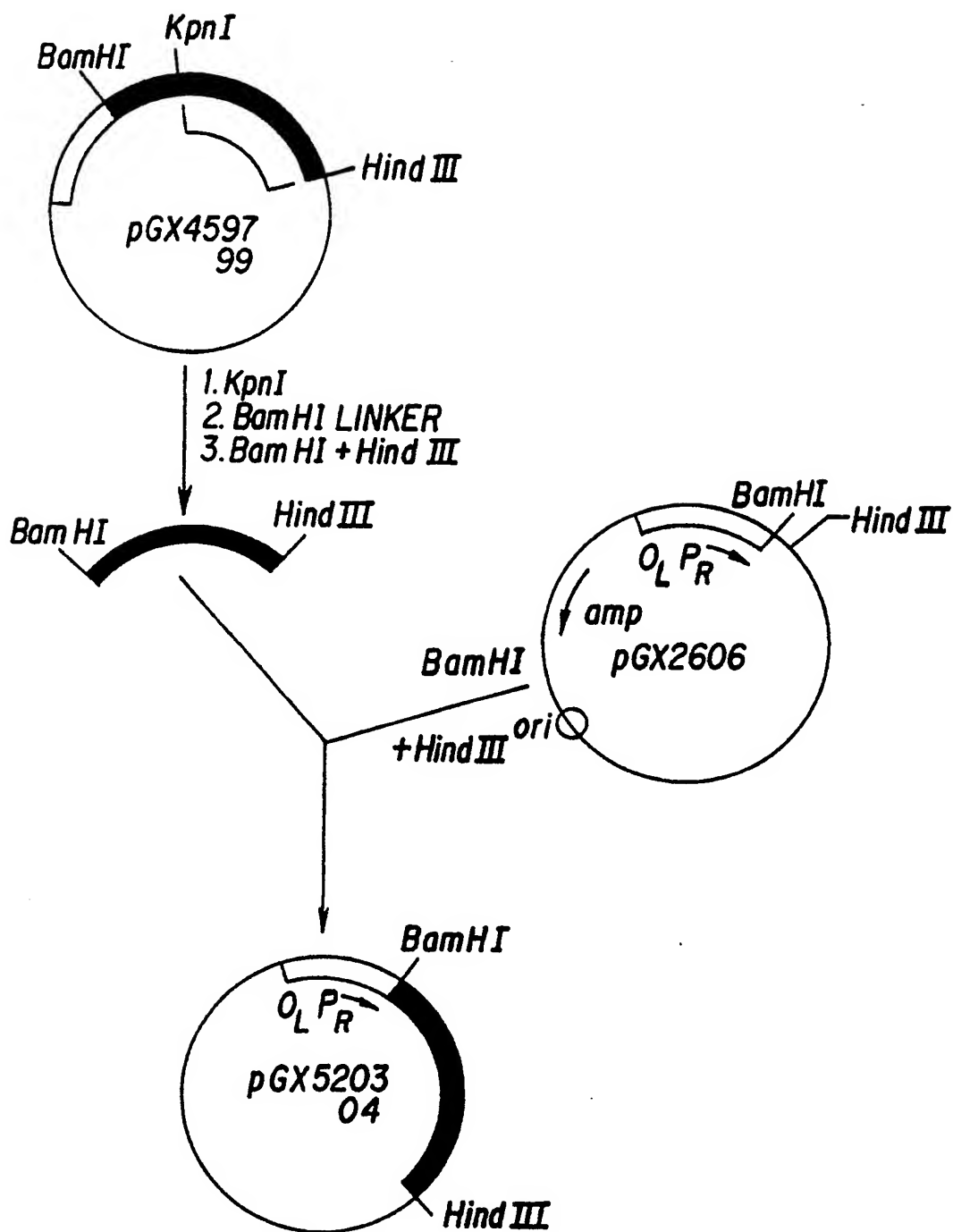


FIG. 13

PROTEIN G VARIAT TYPE 1

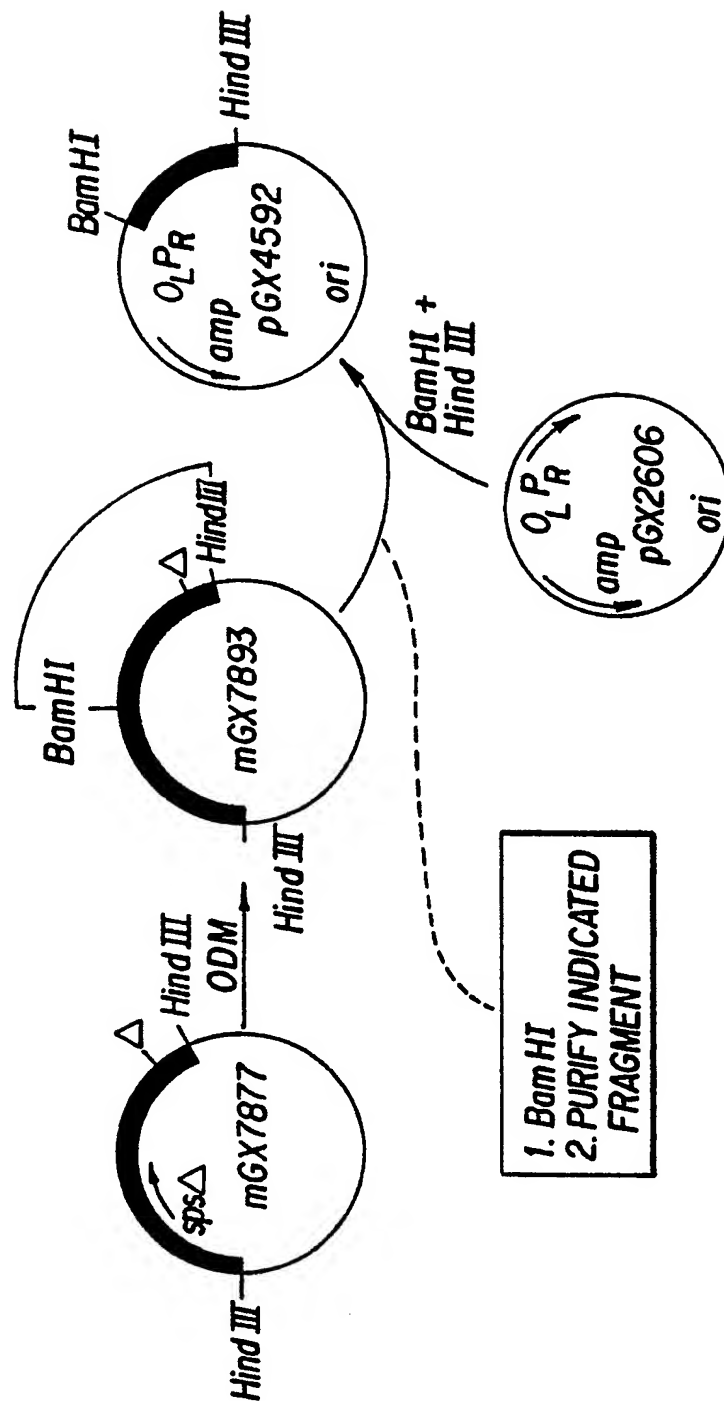


FIG.14

PROTEIN G VARIANT TYPE 5

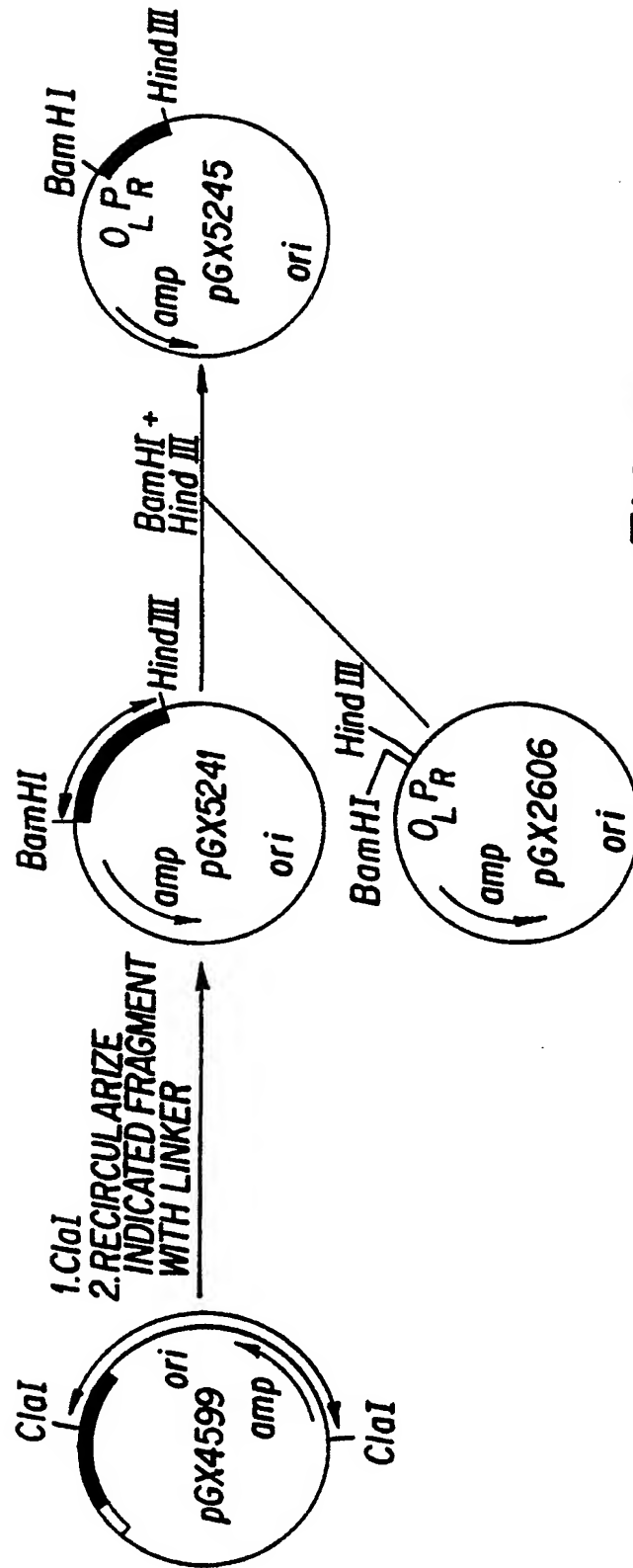


FIG. 15

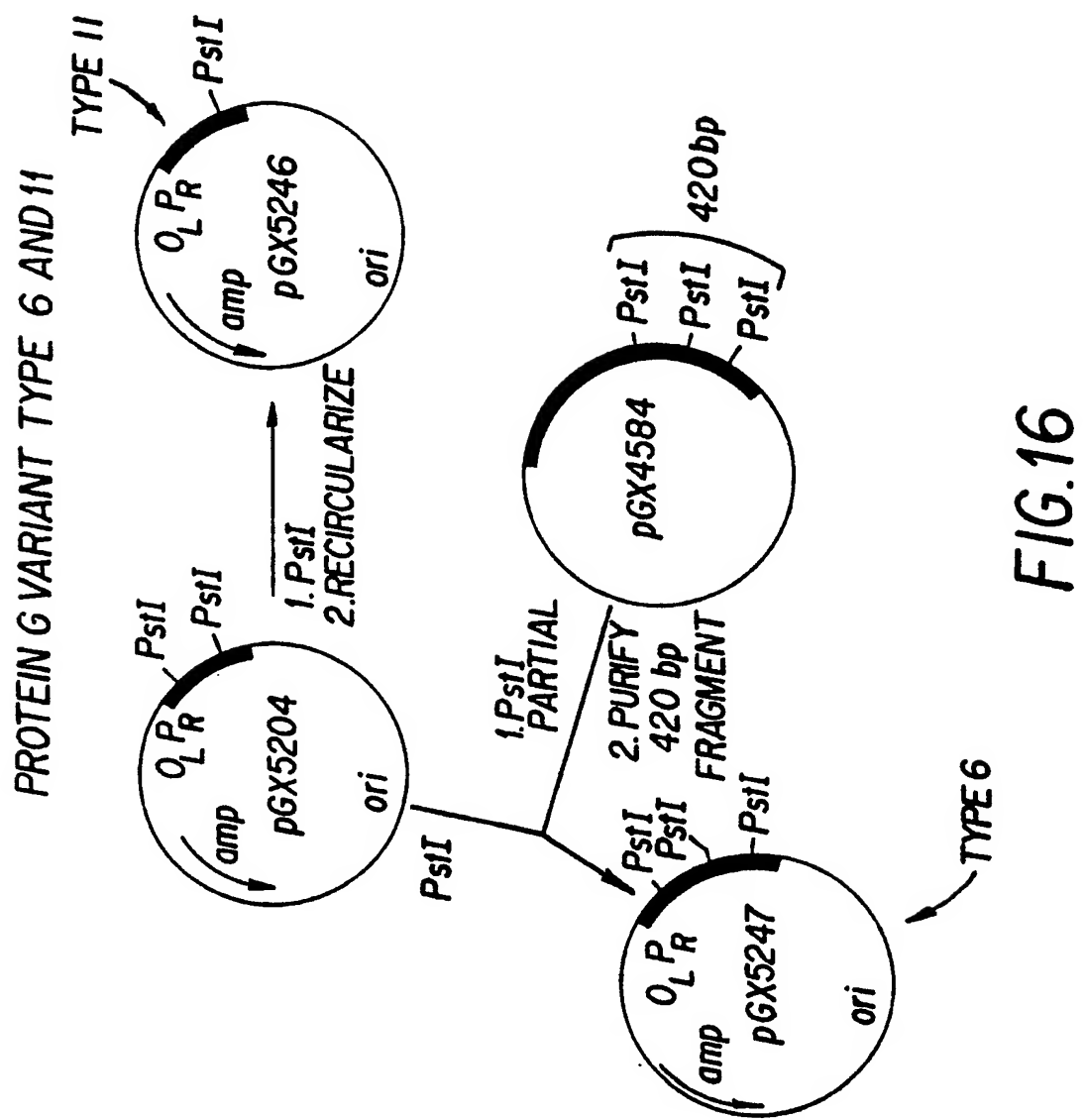


FIG.16

PROTEIN G VARIANT TYPE 7

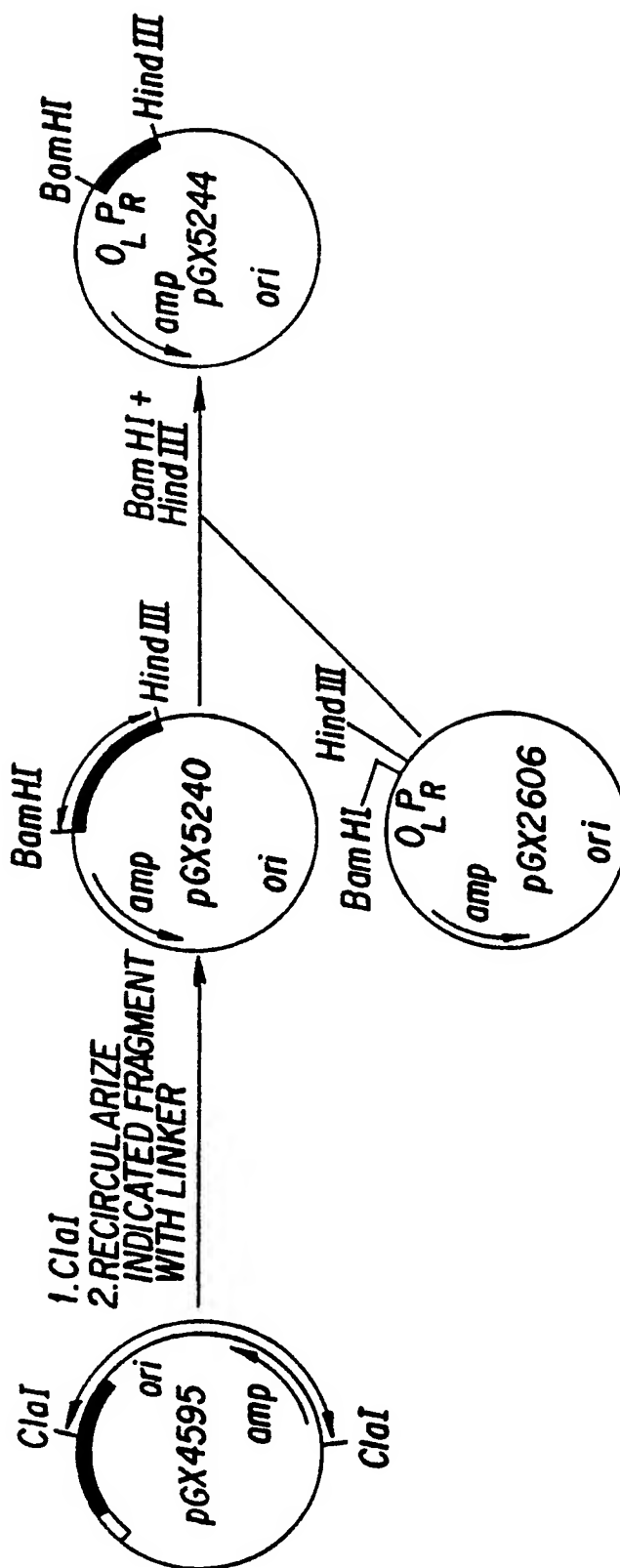


FIG.17

PROTEIN G VARIANT TYPE 8,9

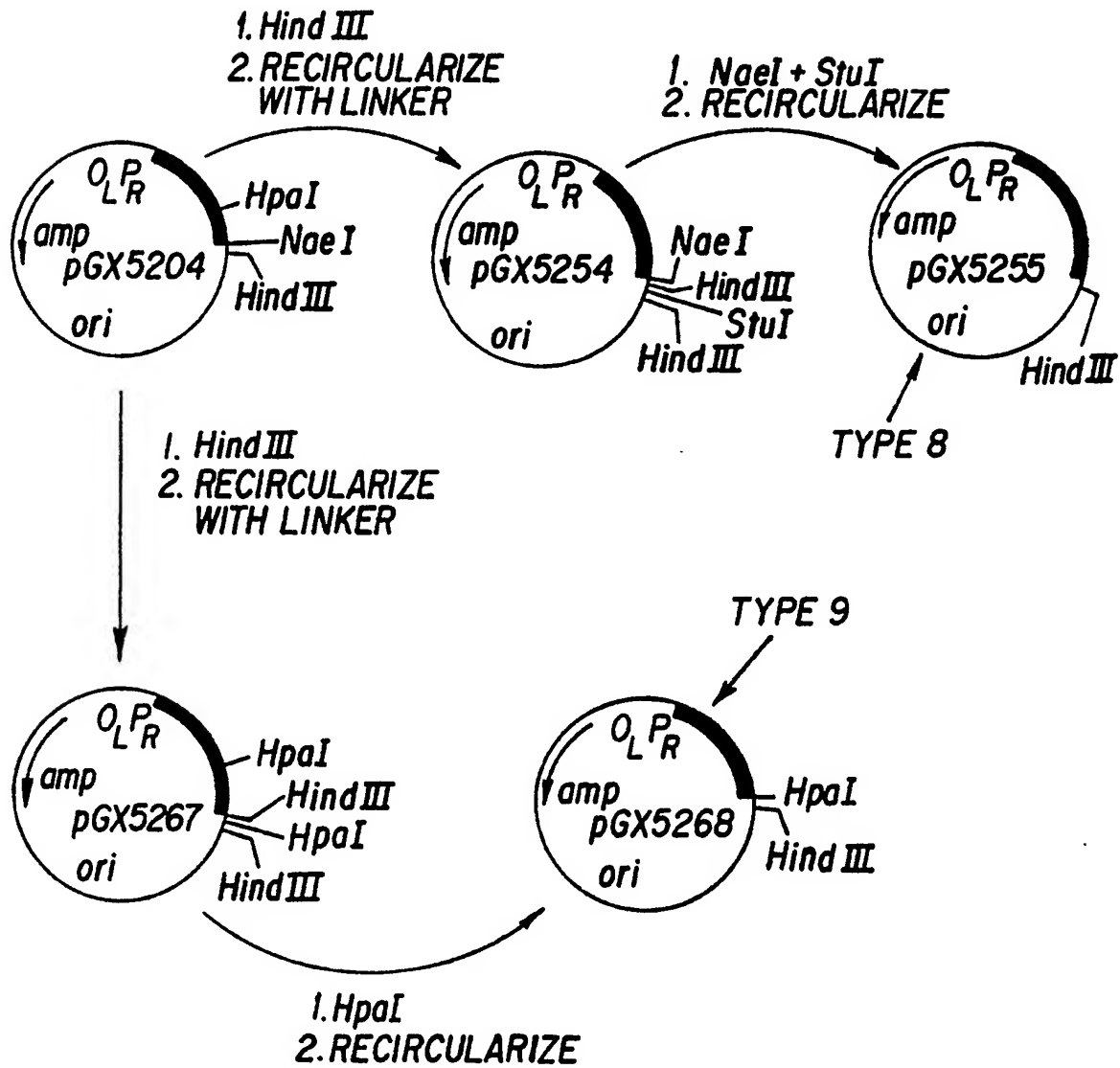
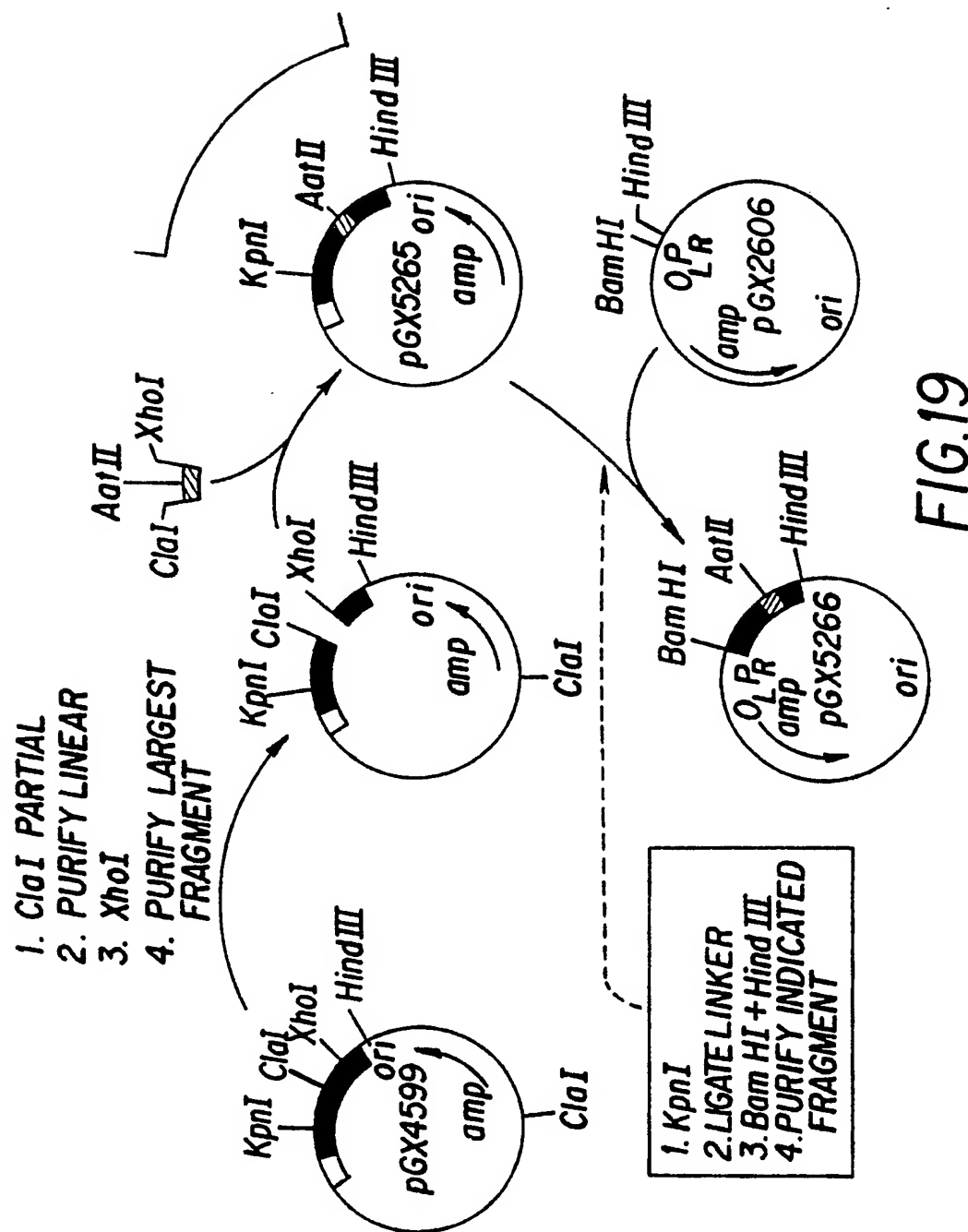


FIG.18





European Patent
Office

EUROPEAN SEARCH REPORT

Application Number

EP 90 30 5415

DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int. Cl.5)
X	WO-A-8 810 306 (GENEX CORP.) * The whole document *	1-17,23 -29	C 07 K 13/00 C 12 N 15/31
Y	---	18-22	C 07 K 3/20
Y	MOLECULAR IMMUNOLOGY, vol. 25, no. 2, 1988, pages 121-126, Pergamon Journals Ltd, GB; M. ERNTELL et al.: "Streptococcal protein G has affinity for both Fab- and Fc-fragments of human IgG" * Page 123, column 2, lines 51-65; page 125, column 2 *	18	
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Y	J. CLIN. CHEM. BIOCHEM., vol. 26, no. 9, 1988, pages 559-568, Walter de Gruyter & Co., Berlin, DE; D. JOSIC et al.: "Isolation of immunoglobulins and their use in immunoaffinity HPLC" * Page 566, column 1, line 25 - page 567, column 1, line 30 *	19	
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Y	THE JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 261, no. 22, 5th August 1986, pages 10240-10247, The American Society for Biological Chemists, Inc., US; B. AKERSTROM et al.: "A physicochemical study of protein G, a molecule with unique immunoglobulin G-binding properties" * Page 10242, table III; page 10243, figure 8; page 10244, figure 10 *	20-22	TECHNICAL FIELDS SEARCHED (Int. Cl.5) C 12 N
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	-/-		
The present search report has been drawn up for all claims			
Place of search THE HAGUE		Date of completion of the search 22-08-1990	Examiner SKELLY J.M.
CATEGORY OF CITED DOCUMENTS			
X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	



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P,X	BIOLOGICAL ABSTRACTS, vol. 90, abstract no. 15721, Biological Abstracts Inc., Philadelphia, PA, US; C.R. GOWARD et al.: "Expression and purification of a truncated recombinant streptococcal protein G", & BIOCHEM. J. 267(1). 1990. 171-178 * Abstract * ---	1-17,23 -29	
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			TECHNICAL FIELDS SEARCHED (Int. Cl.5)
The present search report has been drawn up for all claims			
Place of search THE HAGUE		Date of completion of the search 22-08-1990	Examiner SKELLY J.M.
CATEGORY OF CITED DOCUMENTS			
X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	